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(54) Title: CELLULAR ARRAYS FOR RAPID MOLECULAR PROFILING			
(57) Abstract <p>A method is disclosed for rapid molecular profiling of tissue or other cellular specimens by placing a donor specimen in an assigned location in a recipient array, providing copies of the array, and performing a different biological analysis of each copy. In one embodiment, the copies of the array are formed by placing elongated specimens in a three dimensional matrix, and cutting sections from the matrix to form multiple copies of a two dimensional array that can then be subjected to the different biological analyses. Alternatively, the array can be formed from cell suspensions such that identical multiple copies of an array are formed, in which corresponding positions in the copies of the array have samples from the same or similar specimen. The results of the different biological analyses are compared to determine if there are correlations between the results of the different biological analyses at each assigned location. In some embodiments, the specimens may be tissue specimens from different tumors, which are subjected to multiple parallel molecular (including genetic and immunological) analyses. The results of the parallel analyses are then used to detect common molecular characteristics of the tumor type, which can subsequently be used in the diagnosis or treatment of the disease. The biological characteristics of the tissue can be correlated with clinical or other information, to detect characteristics associated with the tissue, such as susceptibility or resistance to particular types of drug treatment. Other examples of suitable tissues which can be placed in the matrix include tissue from transgenic or model organisms, or cellular suspensions (such as cytological preparations or specimens of liquid malignancies or cell lines).</p>			

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## CELLULAR ARRAYS FOR RAPID MOLECULAR PROFILING

### FIELD OF THE INVENTION

The present invention concerns the microscopic, histologic and/or molecular analysis  
5 of tissue or other cellular specimens.

### BACKGROUND OF THE INVENTION

Biological mechanisms of many diseases have been clarified by microscopic  
examination of tissue specimens. Histopathological examination has also permitted the  
10 development of effective medical treatments for a variety of illnesses. In standard anatomical  
pathology, a diagnosis is made on the basis of cell morphology and staining characteristics. Tumor  
specimens, for example, can be examined to characterize the tumor type and predict the  
aggressiveness of the tumor. Although this microscopic examination and classification of tumors  
has improved medical treatment, the microscopic appearance of a tissue specimen stained by  
15 standard methods (such as hematoxylin and eosin) can often only reveal a limited amount of  
diagnostic or molecular information.

Recent advances in molecular medicine have provided an even greater opportunity to  
understand the cellular mechanisms of disease, and select appropriate treatments with the greatest  
likelihood of success. Some hormone dependent breast tumor cells, for example, have an increased  
20 expression of estrogen receptors on their cell surfaces, which indicates that the patient from whom  
the tumor was taken will likely respond to certain anti-estrogenic drug treatments. Other diagnostic  
and prognostic cellular changes include the presence of tumor specific cell surface antigens (as in  
melanoma), the production of embryonic proteins (such as  $\alpha$ -fetoprotein in liver cancer and  
carcinoembryonic glycoprotein antigen produced by gastrointestinal tumors), and genetic  
25 abnormalities (such as activated oncogenes in tumors). A variety of techniques have evolved to  
detect the presence of these cellular abnormalities, including immunophenotyping with monoclonal  
antibodies, in situ hybridization with probes, and DNA amplification using the polymerase chain  
reaction (PCR).

The development of new molecular markers of clinical importance has been impeded  
30 by the slow and tedious process of evaluating biomarkers in large numbers of clinical specimens.  
For example, hundreds of tissue specimens representing different stages of tumor progression have  
to be evaluated before the importance of a given marker can be assessed. Since the number of  
antibodies, as well as probes for mRNA or DNA targets is increasing rapidly, only a small fraction  
of these can ever be tested in large numbers of clinical specimens.

35 Battifora et al. proposed in *Lab. Invest.* 55:244-248 (1986), and in U.S. Patent No.  
4,820,504, that multiple tissue specimens may be grouped together on a single slide to enable the  
specimens to be simultaneously screened by application of a single drop of hybridoma supernatant.

The specimens were prepared by using a hand-held razor blade to cut deparaffinized and dehydrated tissue specimens into slices, which were then bundled together randomly, wrapped in a sausage casing, and re-embedded in paraffin. This technique required a high degree of manual dexterity, and incorporated samples into a composite block in a manner that made it difficult to find and identify particular specimens of interest.

A modification of this process was disclosed by Wan et al., *J. Immunol. Meth.* 103:121-129 (1987), and Furmanski et al. in U.S. Patent No. 4,914,022, in which cores of paraffin embedded tissue were obtained from standard tissue blocks. The cores were softened and straightened by manually rolling them on a warm surface, and then bundled inside a conventional drinking straw. This method was said to be suitable for simultaneous histologic testing of multiple tissue specimens, for example in the characterization of monoclonal antibodies. The technique of Miller and Groothuis, *A.J.C.P.* 96:228-232 (1991) similarly rolled tissue strips into "logs" from which transverse sections were taken to be embedded in paraffin. The straw and log techniques, however, were labor intensive, required a high degree of manual dexterity, and also randomly arranged the samples in a manner that complicated the identification of specimens of interest.

Battifora and Mehta, *Lab. Invest.* 63:722-724 (1990), and U.S. Patent No. 5,002,377, attempted to overcome some of the problems of random placement by cutting specimens into a plurality of narrow strips, which were individually positioned in parallel rectangular grooves in a mold. The tissue strips were embedded in agar gel that was poured into the grooves to produce a plate-like member with a series of ridges. Several of the ridged plates were stacked together and embedded in paraffin to form a tissue block. A similar approach was proposed by Sundblad, *A.J.C.P.* 102:192-193 (1993), in which the tissue strips were placed in triangular wedges instead of rectangular grooves. Slicing the tissue, assembling it into rows, and embedding it in several steps to form the block was a time-consuming method that reduced the efficiency of examining a large number of tissue specimens.

All of these techniques have been inadequate for the efficient preparation of an array of tissue specimens that can be used for rapid parallel analysis of a variety of independent molecular markers. The number of tissues that can be positioned in a block is very limited with the aforementioned techniques, and the configuration of the tissues in the block is not standardized, which makes it difficult to develop automated analysis methods, as well as trace the same tissue through multiple consecutive sections. Furthermore, these techniques have only been applied to testing antibodies, which usually are not available in the early phases of investigations of new genes. This inefficiency has been a significant problem in fields such as cancer research, because cancer development and progression is a multi-step process that involves sequential losses, rearrangements and amplifications of several chromosomal regions and multiple genes. These events lead to a dysregulation of critical signal transduction pathways for cell growth, death, and differentiation. The details of this complex process remain incompletely understood, partly because

high-throughput strategies and techniques for analyzing such genetic changes in large numbers of uncultured human tumors have not been available.

For example, simultaneous analysis of several genes within the same or related signal transduction pathways may be necessary to pinpoint critical, rate-limiting steps in the dysregulation of cancer cell growth. Furthermore, analysis of structural and numerical changes affecting several chromosomes, loci and genes at the same time may be needed to understand the patterns of accumulation of genetic changes in different stages of the cancer progression. Finally after novel genes and genetic changes of potential importance in cancer have been identified, substantial additional research is usually required to determine the diagnostic, prognostic and therapeutic significance of these molecular markers in clinical oncology.

Since the amount of tissue often becomes rate limiting for such studies, the ability to efficiently procure, fix, store and distribute tissue for molecular analysis in a manner that minimizes consumption of often unique, precious tumor specimens is important.

While the concept of nucleic acid hybridization is not new and has been used routinely in biomedical laboratories for several years, a new technology referred to as DNA microarray technology or Gene Chip technology, has increased the rate at which information may be obtained from cells, tissues, or other experiments. Such high-throughput informational biotechnology has been described, for instance, in Schena et al., *Science*, 270:467-470, 1995; Schena, *BioEssays*, 18(5):427-431, 1996; Soares, *Cur. Opp in Biotechnol.*, 8:542-546, 1997; Ramsay, *Nature Biotechnology*, 16: 14-44, 1998; Service, *Science*, 282:396-399, 1998 and in U.S. Patent No. 5,700,637.

Schena et al., 1995 describes a microarray composed of 45 cloned Arabidopsis cDNA's that was used to quantitatively measure expression of corresponding genes using fluorescent-labeled Arabidopsis mRNA probes. Schena, 1996 reviews cDNA arrays that may be probed with fluorescent-labeled mRNA probe. and discusses measurement of differential expression using two different samples labeled with two different colored fluorescent labels. Soares, 1997, discusses cDNA microarrays used for the identification of up-regulated and down-regulated genes important in cancer, and the use of such arrays to identify gene therapy targets. Ramsey, 1998 and Service, 1998 review different micro-arrays used for various diagnostic and therapeutic purposes, such as for the identification of amplified genes, polymorphism screening, mapping of genomic DNA clones, and comparative genomic hybridization.

These references identify two basic types of array, those in which sample DNA (for instance, entire genomes, or representative sequences from those genomes) are immobilized to a support and exposed to labeled probes; and those in which the target sequences, for instance an array of oligonucleotides, is synthesized or immobilized on a support and exposed to labeled sample DNA. In each case, the probe may contain a known copy number of a known gene, and the sample

DNA binds the probe such that the degree of binding is indicative of the presence or absence of a particular gene, or the up-regulation or down-regulation of the gene.

### SUMMARY OF THE INVENTION

5           The present invention provides a method of high-throughput large-scale molecular profiling of tissue specimens (such as tumors) with minimal tissue requirements, in a manner that allows rapid parallel analysis of biological characteristics, such as molecular characteristics (for example gene dosage and expression) from hundreds of morphologically controlled tumor specimens. These objects are achieved by a method of parallel analysis of tissue specimens, in  
10       which a plurality of donor specimens are placed in assigned locations in a recipient array, and a plurality of sections are obtained from the recipient array so that each section contains a plurality of donor specimens that maintain their assigned locations.

          A different tissue analysis (such as a histological, immunologic or molecular analysis) is performed on each section, to determine if there are correlations between the results of the  
15       different analyses at corresponding locations of the array. In particular embodiments, the donor specimen is obtained by boring an elongated sample, such as a cylindrical core, from donor tissue, and placing the donor specimen in a receptacle of complementary shape, such as a cylindrical core, in the recipient array. Analyses that may be performed on the donor specimens include all kinds of histological, clinicopathological, and molecular analyses, such as histochemical or immunological  
20       analysis, nucleic acid hybridization, or extraction of proteins, and DNA and RNA molecular analysis, including PCR analyses, such as in situ PCR and in situ RT-PCR.

          In a more particular embodiment of the method, a recipient block is formed from a rigid embedding medium such as paraffin that can be cut with a punch or microtome, and a separate donor block is also formed by embedding a biological specimen in the embedding medium.  
25       Cylindrical receptacle cores are bored in the recipient block to form an array of receptacles at fixed positions, and cylindrical donor sample cores are obtained from the embedded biological specimen in the donor block. The donor sample cores are then placed in the cylindrical receptacles at assigned locations in the array, and the recipient block is sliced to obtain a cross-section of the donor sample cores in the array, without disrupting the assigned array locations. A different  
30       biological analysis may be performed on each section, for example by using different monoclonal antibodies that recognize distinct antigens, or a combination of antigenically distinct monoclonal antibodies and nucleic acid (e.g. RNA and DNA) probes on sequential sections.

          The result of each distinct tissue analysis in each position of the array is compared, for example to determine if a tissue that expresses an estrogen receptor also has evidence that a  
35       particular oncogene has been activated. The presence or absence of the estrogen receptor and oncogene can then be correlated with clinical or pathological information about the tissue (such as the presence of metastatic disease or the histological grade of a tumor). This simultaneous parallel

analysis of multiple specimens helps clarify the inter-relationship of multiple molecular and clinical characteristics of the tissue.

The invention also includes a method of obtaining small elongated samples of tissue from a tissue specimen, such as a tumor, and subjecting the specimen to laboratory analysis, such as histological or molecular analysis. The elongated tissue sample can be taken from a region of interest of the tissue specimen. In a disclosed embodiment, the sample is a cylindrical sample punched from the tissue specimen, wherein the cylindrical specimen is about 1-4 mm long, and has a diameter of about 0.1-4 mm, for example about 0.3-2.0 mm. In specific embodiments, the cylinder diameter is less than about 1.0 mm, for example 0.6 mm. The sample may be preserved in a manner (such as ethanol fixation) that does not interfere with analysis of nucleic acids, and the sample can therefore be subjected to any type of molecular analysis, such as any type of molecular analysis based on isolated DNA or RNA embedded. Routinely fixed archival tissue specimens can also be used for most analyses, including immunological and in situ hybridization.

In an alternative embodiment, cells from a cell line of interest can be placed in the array, and analyzed in the same manner as the tissue specimens.

The invention also includes an apparatus for preparing specimens for parallel analysis of sections of biological material arrays. The apparatus includes a platform, a tissue donor block on the platform, and a punch that punches or bores a tissue specimen from the donor block. The platform can also carry a recipient block in which the punch forms an array of receptacles at selected positions. Each receptacle can be positioned so that a tissue specimen can be expelled from the reciprocal punch into the receptacle. An x-y positioning device incrementally moves the punch or recipient block with respect to one another as the punch reciprocates, to form the receptacle array. The x-y positioning device also aligns sequential receptacles of the recipient block with the punch to deliver tissue specimens from the punch into the receptacle. A stylet may be introduced into the punch to expel the contents of the punch, which may be either material (such as paraffin) from the recipient block, or tissue from the donor block. Regions of interest of the tissue specimen are located by positioning a stained section slide (such as a hematoxylin and eosin stained slide) cut from the original block over the donor block, to align structures of interest in the thin section slide with corresponding tissue specimen regions in the donor block.

The invention also includes a computer implemented system for parallel analysis of consecutive sections of tissue arrays, in which an x-y positioning platform moves a tray (or moves a punch) to a plurality of coordinates that correspond to positions in a recipient block array. A receptacle punch then punches a receptacle core from a recipient block on the positioning platform, and a stylet expels the receptacle core from the receptacle punch. A donor punch (which may be the same or separate from the recipient punch) punches a donor specimen from a donor block on the positioning platform, and a stylet expels the donor specimen from the donor punch into the receptacle as the donor punch is introduced into the receptacle. The donor specimen suitably has a

diameter that is substantially the same as the diameter of the receptacle, so that the donor specimen fits securely in the receptacle. The computer system identifies the tissue by its location in the recipient array, so that when the donor block is sectioned a corresponding position in each sectional array will contain tissue from the identical donor specimen.

5           The invention also includes methods that combine tissue microarray technology with other technologies, such as high-throughput genomics, to identify molecular characteristics, such as structural changes in genes or proteins, copy number or expression alterations of genes, with disease prognosis or therapy outcome, to identify novel targets for gene prevention, early diagnosis, disease classification, or prognosis, and to identify therapeutic agents. Such high-throughput  
10 technologies include cDNA and genomic sequencing, serial analysis of gene expression (SAGE), representational difference analysis (RDA), differential display and related PCR-based technologies, hybridization-based sequencing, subtractive cDNA or genomic hybridizations, cDNA arrays, CGH arrays, electrophoretic or other separation methods for DNA or protein, yeast two-hybrid technology or related techniques of molecular biology. Similarly, information obtained or  
15 deduced from electronic databases, such as those containing DNA or protein sequence information, can be used to develop probes or reagents that can be tested with the tissue array technology.

          The use of tissue arrays alone or in combination with other array techniques can provide information about the frequency of a multitude of genetic alteration or gene expression patterns (including normal gene expression patterns) in a variety of tissue types (such as different  
20 types of tumors), and in tissue of a particular histological type (such as a tumor of a specific type, such as intraductal breast cancer), as well as the tissue distribution of molecular markers tested.

          In one specific embodiment of the combined DNA and tissue arrays, the DNA array may be a cDNA or genomic microarray chip that allows a plurality (hundreds, thousands or even more) of different nucleic acid sequences to be affixed to the surface of a support to form an array.  
25       Such a chip may, for instance carry an array of cDNA clones, oligonucleotides, or large-insert genomic P1, BAC or PAC clones. These arrays enable the analysis of hundreds of genes or genomic fragments at once to determine their expression or copy number in a test specimen.

          A high-throughput DNA chip can be used together with high-throughput tissue array technology. Such hybrid inventions include using a DNA array to screen a limited number of  
30 tumor samples for expression or copy number of one or more (for example thousands of) specific genes or DNA sequences. Probes containing the gene of interest may then be used to screen a tissue microarray that contains many different tissue specimens (such as a variety of breast tumors or prostate tumors) to determine if the identified gene or genetic locus is similarly altered in these tumors. For instance, a cDNA chip can be used to screen a human breast cancer cell line, to  
35 identify one or more genes that are overexpressed or amplified in that particular breast cancer. A probe, corresponding to the identified gene, would then be used to probe a tissue array containing a plurality of tissue samples from different breast cancers, or even tumors of different types (such as



lung or prostate cancer). Such a probe could be made by labeling the identical clone used in the DNA array (for example with a fluorescent or radioactive marker). The presence of the gene in related (or unrelated) tumors would be revealed by the pattern of hybridization of the probe to the tissue array.

5 Another embodiment includes a method of preparing a diagnostic tumor-specific gene array.

The foregoing and other objects, features, and advantages of the invention will become more apparent from the following detailed description of particular embodiments which proceeds with reference to the accompanying drawings.

10

### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic perspective view of a first embodiment of the punch device of the present invention, showing alignment of the punch above a region of interest of donor tissue in a donor block.

15 FIG. 2 is a view similar to FIG. 1, but in which the punch has been advanced to obtain a donor specimen sample.

FIG. 3 is a schematic, perspective view of a recipient block into which the donor specimen has been placed.

FIGS. 4-8 illustrate steps in the preparation of thin section arrays from the recipient block.

20 FIG. 9 is a perspective view of a locking device for holding a slide mounted specimen above the tissue in the donor block to locate a region of interest.

FIG. 10A is a view of an H&E stained, thin section tissue array mounted on a slide for microscopic examination.

25 FIG. 10B is a magnified view of a portion of the slide in FIG. 10A, showing results of erbB2 mRNA in situ hybridization on a tissue array from the region in the small rectangle in FIG. 10A.

FIG. 10C is an electrophoresis gel showing that high molecular weight DNA and RNA can be extracted from the breast cancer specimens fixed in cold ethanol.

30 FIG. 10D is an enlarged view of one of the tissue samples of the array in FIG. 10A, showing an immunoperoxidase staining for the erbB2 antigen.

FIG. 10E is a view similar to FIG. 10D, showing high level erbB2 gene amplification detected by fluorescent in situ hybridization (FISH) of tissue in the array by an erbB2 DNA probe.

FIGS. 11A, 11B, 11C and 11D are schematic views illustrating an example of parallel analysis of arrays obtained by the method of the present invention.

35 FIG. 12 is an enlarged view of a portion of FIG. 11.

FIG. 13 is a top view of a second embodiment of a device for forming the arrays of the present invention.

FIG. 14 is a front view of the device shown in FIG. 13, illustrating the formation of a receptacle in a recipient block with a recipient punch.

FIG. 15 is a view similar to FIG. 14, but showing expulsion of a plug from the recipient punch into a discard tray.

5        FIG. 16 is a view showing a donor punch obtaining a tissue specimen from a donor block.

FIG. 17 is a view showing insertion of the donor tissue into a receptacle of the recipient block.

FIG. 18 is an enlarged view of the donor punch aligned above a structure of interest in the donor block, which is shown in cross-section.

10        FIG. 19 is an enlarged cross-sectional view of the recipient punch, while FIG. 20 is a similar view of the donor punch, illustrating the relative cross-sectional diameters of the two punches.

FIG. 21 is a cross-sectional view of the recipient block with the donor specimens arranged in the recipient array, and with lines of microtome sections of the recipient block being shown.

15        FIG. 22 is a schematic view of a computer system in which the method of the present invention can be implemented.

FIG. 23 is an algorithm illustrating an example of the computer implemented method of the present invention.

20        FIG. 24 is a schematic representation of a gCGH microarray that contains 31 target loci that have been reported to undergo amplification in cancer. Circles around target loci indicate amplifications found in the breast cancer cell lines tested in this study.

FIG. 25 is a digital representation of the results of a chromosomal CGH analysis showing high level amplifications in Sum-52 breast cancer cells at 10q25-q26 and at 7q21-q22, a genosensor CGH analysis indicating high level amplifications of the MET (7q21) and FGFR2 (10q25) oncogenes, and a FISH analysis showing amplification of FGFR2 (at 10q25).

25        FIG. 26 is a schematic diagram of a breast cancer tissue microarray, as well as a digital image of a hybridization, showing that FGFR2 was amplified in 4.5% of the tumor samples in the breast cancer tissue microarray.

FIG. 27 is a schematic representation of the combination of the DNA array and the tissue array, showing that the DNA array can probe a single tumor with hundreds of probes, while the tissue array technology can conversely probe specimens from hundreds of tumors with a single probe.

30        FIG. 28 is a schematic diagram representing the combination of the tissue array technology with cDNA and/or CGH arrays.

35

## DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

### Definitions

By "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation).

5 A "gene amplification" is an increase in the copy number of a gene, as compared to the copy number in normal tissue. An example of a genomic amplification is an increase in the copy number of an oncogene. A "gene deletion" is a deletion of one or more nucleic acids normally present in a gene sequence, and in extreme examples can include deletions of entire genes or even portions of chromosomes.

10 A "genomic target sequence" is a sequence of nucleotides located in a particular region in the human genome that corresponds to one or more specific loci, including genetic abnormalities, such as a nucleotide polymorphism, a deletion, or an amplification.

A "genetic disorder" is any illness, disease, or abnormal physical or mental condition that is caused by an alteration in one or more genes or regulatory sequences (such as a mutation,  
15 deletion or translocation).

A "nucleic acid array" refers to an arrangement of nucleic acid (such as DNA or RNA) in assigned locations on a matrix, such as that found in cDNA or CGH arrays.

A "microarray" is an array that is miniaturized so as to require microscopic examination for visual evaluation.

20 A "DNA chip" is a DNA array in which multiple DNA molecules (such as cDNAs) of known DNA sequences are arrayed on a substrate, usually in a microarray, so that the DNA molecules can hybridize with nucleic acids (such as cDNA or RNA) from a specimen of interest. DNA chips are further described in Ramsay, *Nature Biotechnology* 16: 40-44, 1998, which is incorporated by reference.

25 "Comparative Genomic Hybridization" or "CGH" is a technique of differential labeling of test DNA and normal reference DNA, which are hybridized simultaneously to chromosome spreads, as described in Kallioniemi et al., *Science* 258:818-821, 1992, which is incorporated by reference.

"Gene expression microarrays" refers to microscopic arrays of cDNAs printed on a  
30 substrate, which serve as a high density hybridization target for mRNA probes, as in Schena, *BioEssays* 18:427-431, 1996, which is incorporated by reference.

"Serial Analysis of Gene Expression" or "SAGE" refers to the use of short sequence tags to allow the quantitative and simultaneous analysis of a large number of transcripts in tissue, as described in Velculescu et al., *Science* 270:484-487, 1995, which is incorporated by reference.

35 "High throughput genomics" refers to application of genomic or genetic data or analysis techniques that use microarrays or other genomic technologies to rapidly identify large

numbers of genes or proteins, or distinguish their structure, expression or function from normal or abnormal cells or tissues.

A "tumor" is a neoplasm that may be either malignant or non-malignant. "Tumors of the same tissue type" refers to primary tumors originating in a particular organ (such as breast, prostate, bladder or lung). Tumors of the same tissue type may be divided into tumors of different sub-types (a classic example being bronchogenic carcinomas (lung tumors) which can be an adenocarcinoma, small cell, squamous cell, or large cell tumor).

A "cellular" specimen is one which contains whole cells, and includes tissues (which are aggregations of similarly specialized cells, united in the performance of a particular function. Examples include cells from the skin, breast, prostate, blood, testis, ovary and endometrium.

A "cellular suspension" is a liquid in which cells are dispersed, and may include a uniform or non-uniform suspension. Examples of cellular suspensions are those obtained by fine-needle aspiration from tumor sites, cytology specimens (such as vaginal fluids for preparing Pap smears, washes (such as bronchial washings), urine that contains cells (for example in the detection of bladder cancer), ascitic fluid (for example obtained by abdominal paracentesis), or other body fluids.

A "cytological preparation" is a pathological specimen, such as vaginal fluids, in which a cellular suspension can be converted into a smear or other form for pathological examination or analysis.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be limiting.

#### Embodiment of FIGS. 1-12

A first embodiment of a device for making the microarrays of the present invention is shown in FIGS. 1-2, in which a donor block 30 is shown in a rectangular container 31 mounted on a stationary platform 32 having an L-shaped edge guide 34 that maintains donor container 31 in a predetermined orientation on platform 32. A punch apparatus 38 is mounted above platform 32, and includes a vertical guide plate 40 and a horizontal positioning plate 42. The positioning plate 42 is mounted on an x-y stage (not shown) that can be precisely positioned with a pair of digital micrometers.

Vertical guide plate 40 has a flat front face that provides a precision guide surface against which a reciprocal punch base 44 can slide along a track 46 between a retracted position

shown in FIG. 1 and an extended position shown in FIG. 2. An elastic band 48 helps control the movement of base 44 along this path, and the limits of advancement and retraction of base 44 are set by track member 46, which forms a stop that limits the amplitude of oscillation of base 44. A thin wall stainless steel tube punch 50 with sharpened leading edges is mounted on the flat bottom face of base 44, so that punch 50 can be advanced and retracted with respect to platform 32, and the container 31 on the platform. The hollow interior of punch 50 is continuous with a cylindrical bore through base 44, and the bore opens at opening 51 on a horizontal lip 53 of base 44.

FIG. 1 shows that a thin section of tissue, stained with hematoxylin-eosin or other stains, can be obtained from donor block 30 and mounted on a slide 52 (with appropriate preparation and staining) so that anatomic and micro-anatomic structures of interest can be located in the block 30. Slide 52 can be held above donor block 30 by an articulated arm holder 54 (FIG. 9) with a clamp 56 which securely holds an edge of a transparent support slide 58. Arm holder 54 can articulate at joint 60, to swivel between a first position in which support slide 58 is locked in position above container 31, and a second position in which support slide 58 moves horizontally out of the position shown in FIG. 9 to permit free access to punch 50.

In operation, the rectangular container 31 is placed on platform 32 (FIG. 1) with edges of container 31 abutting edge guides 34 to hold container 31 in a selected position. A donor block 30 is prepared by embedding a gross tissue specimen (such as a three dimensional tumor specimen 62) in paraffin. A thin section of donor block 30 is shaved off, stained, and mounted on slide 52 as thin section 64, and slide 52 is then placed on support slide 58 and positioned above donor block 30 as shown in FIG. 9. Slide 52 can be moved around on support slide 58 until the edges of thin section 64 are aligned with the edges of the gross pathological specimen 62, as shown by the dotted lines in FIG. 9. Arm 54 is then locked in the first position, to which the arm can subsequently return after displacement to a second position.

A micro-anatomic or histologic structure of interest 66 can then be located by examining the thin section through a microscope (not shown). If the tissue specimen is, for example, an adenocarcinoma of the breast, then the location of interest 66 may be an area of the specimen in which the cellular architecture is suggestive of specific features of the cancer, such as invasive and noninvasive components. Once the structure of interest 66 is located, the corresponding region of tissue specimen 62 from which the thin section structure of interest 66 was obtained is located immediately below the structure of interest 66. As shown in FIG. 1, positioning plate 42 can be moved in the x and y directions (under the control of the digital micrometers or a joystick), or the donor block can be moved for larger distances, to align punch 50 in position above the region of interest of the donor block 30, and the support slide 58 is then horizontally pivoted away from its position above donor block 30 around pivot joint 60 (FIG. 9).

Punch 50 is then introduced into the structure of interest in donor block 30 (FIG. 2) by advancing vertical guide plate 40 along track 46 until plate 44 reaches its stop position (which is

preset by apparatus 38). As punch 50 advances, its sharp leading edge bores a cylindrical tissue specimen out of the donor block 30, and the specimen is retained within the punch as the punch reciprocates back to its retracted position shown in FIG. 1. The cylindrical tissue specimen can subsequently be dislodged from punch 50 by advancing a stylet (not shown) into opening 51. The tissue specimen is, for example, dislodged from punch 50 and introduced into a cylindrical receptacle of complementary shape and size in an array of receptacles in a recipient block 70 shown in FIG. 3.

One or more recipient blocks 70 can be prepared prior to obtaining the tissue specimen from the donor block 30. Block 70 can be prepared by placing a solid paraffin block in container 31 and using punch 50 to make cylindrical punches in block 70 in a regular pattern that produces an array of cylindrical receptacles of the type shown in FIG. 3. The regular array can be generated by positioning punch 50 at a starting point above block 70 (for example a corner of the prospective array), advancing and then retracting punch 50 to remove a cylindrical core from a specific coordinate on block 70, then dislodging the core from the punch by introducing a stylet into opening 51. The punch apparatus or the recipient block is then moved in regular increments in the x and/or y directions, to the next coordinate of the array, and the punching step is repeated. In the specific disclosed embodiment of FIG. 3, the cylindrical receptacles of the array have diameters of about 0.6 mm, with the centers of the cylinders being spaced by a distance of about 0.7 mm (so that there is a distance of about 0.05 mm between the adjacent edges of the receptacles).

In a specific example, core tissue biopsies having a diameter of 0.6 mm and a height of 3-4 mm, were taken from selected representative regions of individual "donor" paraffin-embedded tumor blocks and precisely arrayed into a new "recipient" paraffin block (20 mm x 45 mm). H&E-stained sections were positioned above the donor blocks and used to guide sampling from morphologically representative sites in the tumors. Although the diameter of the biopsy punch can be varied, 0.6 mm cylinders have been found to be suitable because they are large enough to evaluate histological patterns in each element of the tumor array, yet are sufficiently small to cause only minimal damage to the original donor tissue blocks, and to isolate reasonably homogenous tissue blocks. Up to 1000 such tissue cylinders, or more, can be placed in one 20 x 45 mm recipient paraffin block. Specific disclosed diameters of the cylinders are 0.1-4.0 mm, for example 0.5-2.0 mm, and most specifically less than 1 mm, for example 0.6 mm. Automation of the procedure, with computer guided placement of the specimens, allows very small specimens to be placed tightly together in the recipient array.

FIG. 4 shows the array in the recipient block after the receptacles of the array have been filled with tissue specimen cylinders. The top surface of the recipient block is then covered with an adhesive film 74 from an adhesive coated tape sectioning system (Instrumedics) to help maintain the tissue cylinder sections in place in the array once it is cut. The array block may be warmed at 37 degrees C. for 15 minutes before sectioning, to promote adherence of the tissue cores

and allow smoothing of the block surface when pressing a smooth, clean surface (such as a microscope slide) against the block surface.

With the adhesive film in place, a 4-8  $\mu$ m section of the recipient block is cut transverse to the longitudinal axis of the tissue cylinders (FIG. 5) to produce a thin microarray section 76 (containing tissue specimen cylinder sections in the form of disks) that is transferred to a conventional specimen slide 78. The microarray section 76 is adhered to slide 78, for example by adhesive on the slide. The film 74 is then peeled away from the underlying microarray member 76 to expose it for processing. A darkened edge 80 of slide 78 is suitable for labeling or handling the slide.

Breast cancer tissue specimens were fixed in cold ethanol to help preserve high-molecular weight DNA and RNA, and 372 of the specimens were fixed in this manner. At least 200 consecutive 4-8  $\mu$ m tumor array sections can be cut from each block providing targets for correlated in situ analyses of multiple molecular markers at the DNA, RNA or protein level, including copy number or expression of multiple genes. This analysis is performed by testing for different gene molecular targets (e.g. DNA or RNA sequences or antigens defined by antibodies) in separate array sections, and comparing the results of the tests at identical coordinates of the array (which correspond to tissue specimens from the same tissue cylinder obtained from donor block). This approach enables measurement of virtually hundreds of molecular characteristics from every tumor, thereby facilitating construction of a large series of correlated genotypic or phenotypic characteristics of uncultured human tumors.

An example of a single microarray 76 containing 645 specimens is shown in FIG. 10A. An enlarged section of the microarray (highlighted by a rectangle in FIG. 10A) is shown in FIG. 10B, in which an autoradiogram of erbB2 mRNA in situ hybridization illustrates that two adjacent specimens in the array demonstrate a strong hybridization signal. FIG. 10C illustrates electrophoresis gels which demonstrate that high molecular weight DNA and RNA can be extracted from breast cancer specimens fixed in ethanol at 4°C overnight.

One of the tissue specimens that gave the fluorescent "positive" signals was also analyzed by immunoperoxidase staining, as shown in FIG. 10D, where it was confirmed (by the dark stain) that the erbB2 gene product was present. A DNA probe for the erbB2 gene was used to perform fluorescent in situ hybridization (FISH). Fig. 10D shows one of the tumor array elements, which demonstrated high level erbB2 gene amplification. The insert in FIG. 10E shows three nuclei with numerous tightly clustered erbB2 hybridization signals and two copies of the centromeric reference probe. Additional details about these assays are given in Examples 1-4 below.

The potential of the array technology of the present invention to perform rapid parallel molecular analysis of multiple tissue specimens is illustrated in FIGS. 11A-11D, where the y-axis of the graphs in FIGS. 11A and 11C corresponds to percentages of tumors in specific groups that

have defined clinicopathological or molecular characteristics. This diagram shows correlations between clinical and histopathological characteristics of the tissue specimens in the micro-array. Each small box in the aligned rows of FIG. 11B represents a coordinate location in the array. Corresponding coordinates of consecutive thin sections of the recipient block are vertically aligned above one another in the horizontally extending rows. These results show that the tissue specimens could be classified into four classifications of tumors (FIG. 11A) based on the presence or absence of cell membrane estrogen receptor expression, and the presence or absence of the p53 mutation in the cellular DNA. In FIG. 11B, the presence of the p53 mutation is shown by a darkened box, while the presence of estrogen receptors is also shown by a darkened box. Categorization into each of four groups (ER-/p53+, ER-/p53-, ER+/p53+ and ER+/p53-) is shown by the dotted lines between FIGS. 11A and 11B, which divide the categories into Groups I, II, III and IV corresponding to the ER/p53 status.

FIG. 11B also shows clinical characteristics that were associated with the tissue at each respective coordinate of the array. A darkened box for Age indicates that the patient is premenopausal, a darkened box N indicates the presence of metastatic disease in the regional lymph nodes, a darkened box T indicates a stage 3 or 4 tumor which is more clinically advanced, and a darkened box for grade indicates a high grade (at least grade III) tumor, which is associated with increased malignancy. The correlation of ER/p53 status can be performed by comparing the top four lines of clinical indicator boxes (Age, N, T, Grade) with the middle two lines of boxes (ER/p53 status). The results of this cross correlation are shown in the bar graph of FIG. 11A, where it can be seen that ER-/p53+ (Group I) tumors tend to be of higher grade than the other tumors, and had a particularly high frequency of myc amplification, while ER+/p53+ (Group III) tumors were more likely to have positive nodes at the time of surgical resection. The ER-/p53- (Group II) showed that the most common gene amplified in that group was erbB2. ER-/p53- (Group II) and ER+/p53- (Group IV) tumors, in contrast, were shown to have fewer indicators of severe disease, thus suggesting a correlation between the absence of the p53 mutation and a better prognosis.

This method was also used to analyze the copy numbers of several other major breast cancer oncogenes in the 372 arrayed primary breast cancer specimens in consecutive FISH experiments, and those results were used to ascertain correlations between the ER/p53 classifications and the expression of these other oncogenes. These results were obtained by using probes for each of the separate oncogenes, in successive sections of the recipient block, and comparing the results at corresponding coordinates of the array. In FIG. 11B, a positive result for the amplification of the specific oncogene or marker (mybL2, 20q13, 17q23, myc, cnd1 and erbB2) is indicated by a darkened box. The erbB2 oncogene was amplified in 18% of the 372 arrayed specimens, myc in 25% and cyclin D1 (cnd1) in 24% of the tumors.



The two recently discovered novel regions of frequent DNA amplification in breast cancer, 17q23 and 20q13, were found to be amplified in 13% and 6% of the tumors, respectively. The oncogene mybL2 (which was recently localized to 20q13.1 and found to be overexpressed in breast cancer cell lines) was found to be amplified in 7% of the same set of tumors. MybL2 was amplified in tumors with normal copy number of the main 20q13 locus, indicating that it may define an independently selected region of amplification at 20q. Dotted lines between FIGS. 11B and 11C again divide the complex co-amplification patterns of these genes into Groups I-IV which correspond to ER-/p53+, ER-/p53-, ER+/p53+ and ER+/p53-.

FIGS. 11C and 11D show that 70% of the ER-/p53+ specimens were positive for one or more of these oncogenes, and that myc was the predominant oncogene amplified in this group. In contrast, only 43% of the specimens in the ER+/p53- group showed co-amplification of one of these oncogenes, and this information could in turn be correlated with the clinical parameters shown in FIG. 11A. Hence the microarray technology of the present invention permits a large number of tumor specimens to be conveniently and rapidly screened for these many characteristics, and analyzed for patterns of gene expression that may be related to the clinical presentation of the patient and the molecular evolution of the disease. In the absence of the microarray technology of the present invention, these correlations are more difficult to obtain.

A specific method of obtaining these correlations is illustrated in FIG. 12, which is an enlargement of the right hand portion of FIG. 11B. The microarray 76 (FIG. 10A) is arranged in sections that contain seventeen rows and nine columns of circular locations that correspond to cross-sections of cylindrical tissue specimens from different tumors, wherein each location in the microarray can be represented by the coordinates (row, column). For example, the specimens in the first row of the first section have coordinate positions (1,1), (1,2), . . . (1,9), and the specimens in the second row have coordinate positions (2,1), (2,2), . . . (2,9). Each of these array coordinates can be used to locate tissue specimens from corresponding positions on sequential sections of the recipient block, to identify tissue specimens of the array that were cut from the same tissue cylinder.

FIG. 12 illustrates one conceptual approach to organizing and analyzing the array, in which the rectangular array may be converted into a linear representation in which each box of the linear representation corresponds to a coordinate position of the array. Each of the lines of boxes may be aligned so that each box that corresponds to an identical array coordinate position is located above other boxes from the same coordinate position. Hence the boxes connected by dotted line 1 correspond to the results that can be obtained by looking at the results at a coordinate position [for example (1,1)] in successive thin sections of the donor block, or clinical data that may not have been obtained from the microarray, but which can be entered into the system to further identify tissue from a tumor that corresponds to that coordinate position. Similarly, the boxes connected by dotted line 10 correspond to the results that can be found at coordinate position (2,1) of the array.

and the boxes connected by dotted line 15 correspond to the results at coordinate position (2,6) of the array. The letters a, b, c, d, e, f, g, and h correspond to successive sections of the donor block that are cut to form the array.

5 By comparing the aligned boxes along line 1 in FIG. 12, it can be seen that a tumor was obtained from a postmenopausal woman with no metastatic disease in her lymph nodes at the time of surgical resection, in which the tumor was less than stage 3, but in which the histology of the tumor was at least Grade III. A tissue block was taken from this tumor and is associated with the recipient array at coordinate position (1,1). This array position was sectioned into eight parallel sections (a, b, c, d, e, f, g, and h) each of which contained a representative section of the  
10 cylindrical array. Each of these sections was analyzed with a different probe specific for a particular molecular attribute. In section a, the results indicated that this tissue specimen was p53+: in section b that it was ER-: in section c that it did not show amplification of the mybL2 oncogene; in separate sections d, e, f, g and h that it was positive for the amplification of 20q13, 17q23, myc, cnd1 and erbB2.

15 Similar comparisons of molecular characteristics of the tumor specimen cylinder that was placed at coordinate position (2,1) can be made by following vertical line 10 in FIG. 12, which connects the tenth box in each line, and corresponds to the second row, first column (2,1) of the array 76 in FIG. 10(A). Similarly the characteristics of the sections of the tumor specimen cylinder at coordinate position (2,6) can be analyzed by following vertical line 15 down through the 15<sup>th</sup> box  
20 of each row. In this manner, parallel information about the separate sections of the array can be performed for all 372 positions of the array. This information can be presented visually for analysis as in FIG. 12, or entered into a database for analysis and correlation of different molecular characteristics (such as patterns of oncogene amplification, and the correspondence of those patterns of amplification to clinical presentation of the tumor).

25 Analysis of consecutive sections from the tumor arrays enables co-localization of hundreds of different DNA, RNA, protein or other targets in the same cell populations in morphologically defined regions of every tumor, which facilitates construction of a database of a large number of correlated genotypic or phenotypic characteristics of uncultured human tumors. Scoring of mRNA in situ hybridizations or protein immunohistochemical staining is also facilitated  
30 with tumor tissue microarrays, because hundreds of specimens can be analyzed in a single experiment. The tumor arrays also substantially reduce tissue consumption, reagent use, and workload when compared with processing individual conventional specimens one at a time for sectioning, staining and scoring. The combined analysis of several DNA, RNA and protein targets provides a powerful means for stratification of tumor specimens by virtue of their molecular  
35 characteristics. Such patterns will be helpful to detect previously unappreciated but important molecular features of the tumors that may turn out to have diagnostic or prognostic utility.

Analysis techniques for observing and scoring the experiments performed on tissue array sections include a bright-field microscope, fluorescent microscope, confocal microscope, a digital imaging system based on a CCD camera, or a photomultiplier or a scanner, such as those used in the DNA chip based analyses.

5           These results show that the very small cylinders used to prepare tissue arrays can in most cases provide accurate information, especially when the site for tissue sampling from the donor block is selected to contain histological structures that are most representative of tumor regions. It is also possible to collect samples from multiple histologically defined regions in a single donor tissue block to obtain a more comprehensive representation of the original tissue, and  
10       to directly analyze the correlation between phenotype (tissue morphology) and genotype. For example, an array could be constructed to include hundreds of tissues representing different stages of breast cancer progression (e.g. normal tissue, hyperplasia, atypical hyperplasia, intraductal cancer, invasive and metastatic cancer). The tissue array technology would then be used to analyze the molecular events that correspond to tumor progression.

15           A tighter packing of cylinders, and a larger recipient block can also provide an even higher number of specimens per array. Entire archives from pathology laboratories can be placed in replicate 500-1000 specimen tissue microarrays for molecular profiling. Using automation of the procedure for sampling and arraying, it is possible to make dozens of replicate tumor arrays, each providing hundreds of sections for molecular analyses. The same strategy and instrumentation  
20       developed for tumor arrays also enables the use of tissue cylinders for isolation of high-molecular weight RNA and DNA from optimally fixed, morphologically defined tumor tissue elements, thereby allowing correlated analysis of the same tumors by molecular biological techniques (such as PCR-based techniques) based on RNA and DNA. When nucleic acid analysis is planned, the tissue specimen is preferably fixed (before embedding in paraffin) in an alcohol based fixative, such as  
25       ethanol or Molecular Biology Fixative (Streck Laboratories, Inc., Omaha, NE) instead of in formalin, because formalin can cross-link and otherwise damage nucleic acid. The tissue cylinder of the present invention provides an ample amount of DNA or RNA on which to perform a variety of molecular analyses.

          The potential of this array technology has been illustrated in FISH analysis of gene  
30       amplifications in breast cancer. FISH is an excellent method for visualization and accurate detection of genetic rearrangements (amplifications, deletions or translocations) in individual, morphologically defined cells. The combined tumor array technology allows FISH to become a powerful, high-throughput method that permits the analysis of hundreds of specimens per day.

#### 35           Embodiment of FIGS. 13-23

          An example of an automated system for high speed preparation of the microarrays is shown in FIGS. 13-23. The system includes a stage 100 having an x drive 102 and a y drive 104,

each of which respectively rotates a drive shaft 106, 108. The shaft 108 moves a specimen bench 110 in a y direction, while the shaft 106 moves a tray 112 on the bench 110 in an x direction. Mounted in a front row of tray 112 are three recipient containers 116, 118 and 120, each of which contains a recipient paraffin block 122, 124 or 126, and a donor container 128 that contains a donor paraffin block 130, in which is embedded a tissue specimen 132. In a back row on the tray are two multi-well donor trays 132, 134 (which contain multiple containers for maintaining specimens in liquid medium), and a discard container 136.

Disposed above stage 100 is a punch apparatus 140 that can move up and down in a z direction. Apparatus 140 includes a central, vertically disposed, stylet drive 142 in which reciprocates a stylet 144. Apparatus 140 also includes an inclined recipient punch drive 146, and an inclined donor punch drive 148. Punch drive 146 includes a reciprocal ram 150 that carries a tubular recipient punch 154 at its distal end, and punch drive 148 includes a reciprocal ram 152 that carries a donor tubular punch 156 at its distal end. When the ram 150 is extended (FIG. 14), recipient punch 154 is positioned with the open top of its tubular bore aligned with stylet 144, and when ram 152 is extended (FIG. 16), donor punch 156 is positioned with the open top of its tubular bore aligned with stylet 144.

The sequential operation of the apparatus 140 is shown in FIGS. 13-17. Once the device is assembled as in FIG. 13, a computer system can be used to operate the apparatus to achieve high efficiency. Hence the computer system can initialize itself by determining the location of the containers on tray 112 shown in FIG. 13. The x and y drives 102, 104 are then activated to move bench 110 and tray 112 to the position shown in FIG. 14, so that activation of ram 150 extends recipient punch 154 to a position above position (1,1) in the recipient block 122. Once punch 154 is in position, apparatus moves downward in the z direction to punch a cylindrical bore in the paraffin of the recipient block. The apparatus 140 then moves upwardly in the z direction to raise punch 154 out of the paraffin recipient block 122, but the punch 154 retains a core of paraffin that leaves a cylindrical receptacle in the recipient block 122. The x-y drives are then activated to move bench 110 and position discard container 136 below punch 154. Stylet drive 142 is then activated to advance stylet 144 into the open top of the aligned punch 154, to dislodge the paraffin core from punch 154 and into discard container 136.

Stylet 144 is retracted from recipient punch 154, ram 150 is retracted, and the x-y drive moves bench 110 and tray 112 to place donor container 128 in a position (shown in FIG. 16) such that advancement of ram 152 advances donor punch 156 to a desired location over the donor block 130. Apparatus 140 is then moved down in the z direction to punch a cylindrical core of tissue out of the donor block 130, and apparatus 140 is then moved in the z direction to withdraw donor punch 156, with the cylindrical tissue specimen retained in the punch. The x-y drive then moves bench 110 and tray 112 to the position shown in FIG. 17, such that movement of apparatus 140 downwardly in the z direction advances donor punch 156 into the receptacle at the coordinate

position (1,1) in block 122 from which the recipient plug has been removed. Donor punch 156 is aligned below stylet 144, and the stylet is advanced to dislodge the retained tissue cylinder from donor punch 156, so that the donor tissue cylinder remains in the receptacle of the recipient block 122 as the apparatus 140 moves up in the z direction to retract donor punch 156 from the recipient array. Ram 152 is then retracted.

This process can be repeated until a desired number of recipient receptacles have been formed and filled with cylindrical donor tissues at the desired coordinate locations of the array. Although this illustrated method shows sequential alternating formation of each receptacle, and introduction of the tissue cylinder into the formed receptacle, it is also possible to form all the receptacles in recipient blocks 122, 124 and 126 as an initial step, and then move to the step of obtaining the tissue specimens and introducing them into the preformed receptacles. The same tissue specimen 132 can be repeatedly used, or the specimen 132 can be changed after each donor tissue specimen is obtained, by introducing a new donor block 130 into container 128. If the donor block 130 is changed after each tissue cylinder is obtained, each coordinate of the array can include tissue from a different tissue specimen.

A positioning device is shown in FIG. 18, which helps locate structures of interest from which donor specimens can be taken. The positioning device includes a support slide 160 that extends between opposing walls of donor container 128, to support a specimen slide 162 on which is mounted a thin stained section of the specimen 132 in donor block 130. Using a microscope mounted on apparatus 140 (the objective of the microscope is shown at 166), microanatomic structures of interest can be found. The correct vertical height of apparatus 140 above the top surface of donor block 130 can be determined by the use of two positioning lights 168, 170 that are mounted to apparatus 140. Light beams 172, 174 are projected from lights 168, 170 at an angle such that the beams coincide at a single spot 176 when vertical height of apparatus 140 above the top surface of the light is at a desired z level. This desired z level will position the punches 152, 154 at an appropriate height to penetrate the surface of block 130 at the desired location, and to a desired depth.

It is advantageous if the tissue cylinders punched from block 130 fit securely in the recipient receptacles that are formed to receive them. If the donor punch 156 has the same inner and outer diameters as the recipient punch 154, then the cylindrical donor tissue specimen will be formed by the inner diameter of the punch, and the recipient receptacle will be formed by the outer diameter of the punch. This discrepancy will provide a receptacle that is slightly larger in diameter than the donor tissue cylinder. Hence, as shown in FIGS. 19 and 20, the recipient punch 154 preferably has a smaller diameter than the donor punch 156. Recipient punch will therefore form a cylindrical receptacle (having a diameter corresponding to the outer diameter of punch 154) that is substantially the same diameter as the tissue specimen cylinder 180, which is formed with a diameter that is determined by the inner diameter of the donor punch 156.

FIG. 21 illustrates a cross-section through the recipient array, once the receptacles 182 have been formed and filled with tissue specimen cylinders 180. Small partitions of paraffin material 122 separate tissue cylinders 180, and the receptacles 182 as illustrated are deeper than the specimen cylinders 180, such that a small clearance is present between the specimen and the bottom of the receptacles. Once the array has been formed, a microtome can be used to cut a thin section S off the top of the block 122, so that the section S can be mounted on a specimen slide 162 (FIG. 18) to help locate structures of interest in the tissue specimen 132. The microtome then also cuts thin parallel sections a, b, c, d, e, f, g, and h that can each be subjected to a different molecular analysis, as already described.

### Exemplary Operating Environment

FIG. 22 and the following discussion are intended to provide a brief, general description of a suitable computing environment in which the invention may be implemented. The invention is implemented in a variety of program modules. Generally, program modules include routines, programs, components, data structures, etc. that perform particular tasks or implement particular abstract data types. The invention may be practiced with other computer system configurations, including hand-held devices, multiprocessor systems, microprocessor-based or programmable consumer electronics, minicomputers, mainframe computers, and the like. The invention may also be practiced in distributed computing environments where tasks are performed by remote processing devices that are linked through a communications network. In a distributed computing environment, program modules may be located in both local and remote memory storage devices.

Referring to FIG. 22, an operating environment for an illustrated embodiment of the present invention is a computer system 220 with a computer 222 that comprises at least one high speed processing unit (CPU) 224, in conjunction with a memory system 226, an input device 228, and an output device 230. These elements are interconnected by at least one bus structure 232.

The illustrated CPU 224 is of familiar design and includes an ALU 234 for performing computations, a collection of registers 236 for temporary storage of data and instructions, and a control unit 238 for controlling operation of the system 220. The CPU 224 may be a processor having any of a variety of architectures including Alpha from Digital; MIPS from MIPS Technology, NEC, IDT, Siemens and others; x86 from Intel and others, including Cyrix, AMD, and Nexgen; 680x0 from Motorola; and PowerPC from IBM and Motorola.

The memory system 226 generally includes high-speed main memory 240 in the form of a medium such as random access memory (RAM) and read only memory (ROM) semiconductor devices, and secondary storage 242 in the form of long term storage mediums such as floppy disks, hard disks, tape, CD-ROM, flash memory, etc. and other devices that store data using electrical, magnetic, optical or other recording media. The main memory 240 also can include video display

memory for displaying images through a display device. Those skilled in the art will recognize that the memory 226 can comprise a variety of alternative components having a variety of storage capacities.

5 The input and output devices 228, 230 also are familiar. The input device 228 can comprise a keyboard, a mouse, a scanner, a camera, a capture card, a limit switch (such as home, safety or state switches), a physical transducer (e.g., a microphone), etc. The output device 230 can comprise a display, a printer, a motor driver, a solenoid, a transducer (e.g., a speaker), etc. Some devices, such as a network interface or a modem, can be used as input and/or output devices.

10 As is familiar to those skilled in the art, the computer system 220 further includes an operating system and at least one application program. The operating system is the set of software which controls the computer system's operation and the allocation of resources. The application program is the set of software that performs a task desired by the user, using computer resources made available through the operating system. Both are resident in the illustrated memory system 226.

15 For example, the invention could be implemented with a Power Macintosh 8500 available from Apple Computer, or an IBM compatible Personal Computer (PC). The Power Macintosh uses a PowerPC 604 CPU from Motorola and runs a MacOS operating system from Apple Computer such as System 8. Input and output devices can be interfaced with the CPU using the well-known SCSI interface or with expansion cards using the Peripheral Component  
20 Interconnect (PCI) bus. A typical configuration of a Power Macintosh 8500 has 72 megabytes of RAM for high-speed main memory and a 2 gigabyte hard disk for secondary storage. An IBM compatible PC could have a configuration with 32 megabytes of RAM for high-speed main memory and a 2-4 gigabyte hard disk for secondary storage.

25 In accordance with the practices of persons skilled in the art of computer programming, the present invention is described with reference to acts and symbolic representations of operations that are performed by the computer system 220, unless indicated otherwise. Such acts and operations are sometimes referred to as being computer-executed. It will be appreciated that the acts and symbolically represented operations include the manipulation by the CPU 224 of electrical signals representing data bits which causes a resulting transformation or reduction of the  
30 electrical signal representation, and the maintenance of data bits at memory locations in the memory system 226 to thereby reconfigure or otherwise alter the computer system's operation, as well as other processing of signals. The memory locations where data bits are maintained are physical locations that have particular electrical, magnetic, or optical properties corresponding to the data bits.

35

### Description of Computer-Array System

A block diagram showing a system for carrying out the invention is shown at FIG. 23.

The hardware is initialized at step 250, for example by determining the position of the punches 154, 156, bench 110, and tray 112. The system may then be configured by the operator at step 252, for example by entering data or prompting the system to find the location (x, y, z coordinates) of the upper right corner of each recipient block 122-126, as well as the locations of trays 130-136. The number of donor blocks, receptacles, operating speed, etc. may also be entered at this time.

At step 254, the system prompts for entry of identifying information about the first donor block 130 that will be placed in tray 128. This identifying information can include accession number information, clinical information about the specimen, and any/or other information that would be useful in analyzing the tumor arrays. At step 256, the operator pushes a select function button, which raises the punches 154, 156 and enables a joystick to move the specimens using the x-y drives. The entered data is displayed at step 258, and approved at 260.

The system then obtains one or more donor specimens from the identified donor block at step 262, and prompts the user for entry of information about the next donor block. If information about another block is entered, the system returns to step 256 and obtains the desired number of specimens from the new block. After a new donor block has been placed in donor container 128, the system also checks the position of the punches at step 268. If information about another block is not entered at step 264, the system moves the donor tray to the reloading position so that a block 130 in the donor tray can be removed. This system is also adaptable to sampling cylindrical biopsies from histologically controlled sites of specimens (such as tumors) for DNA/RNA isolation.

The automated tumor array technology easily allows testing of dozens or hundreds of markers from the same set of tumors. These studies can be carried out in a multi-center setting by sending replicate tumor array blocks or sections to other laboratories. The same approach would be particularly valuable for testing newly discovered molecular markers for their diagnostic, prognostic or therapeutic utility. The tissue array technology also facilitates basic cancer research by providing a platform for rapid profiling of hundreds or thousands of tumors at the DNA, RNA and protein levels, leading to a construction of a correlated database of biomarkers from a large collection of tumors. For example, search for amplification target genes requires correlated analyses of amplification and expression of dozens of candidate genes and loci in the same cell populations. Such extensive molecular analyses of a defined large series of tumors would be difficult to carry out with conventional technologies.

### Examples of Array Technology

Applications of the tissue array technology are not limited to studies of cancer, although the following Examples 1-4 disclose embodiments of its use in connection with analysis of



neoplasms. Array analysis could also be instrumental in understanding expression and dosage of multiple genes in other diseases, as well as in normal human or animal tissues, including tissues from different transgenic animals or cultured cells.

5 Tissue arrays may also be used to perform further analysis on genes and targets discovered from, for example, high-throughput genomics, such as DNA sequencing, DNA microarrays, or SAGE (Serial Analysis of Gene Expression) (Velculescu et al., *Science* 270:484-487, 1995). Tissue arrays may also be used to evaluate reagents for cancer diagnostics, for instance specific antibodies or probes that react with certain tissues at different stages of cancer development, and to follow progression of genetic changes both in the same and in different cancer types, or in diseases other than cancer. Tissue arrays may be used to identify and analyze prognostic markers or markers that predict therapy outcome for cancers. Tissue arrays compiled from hundreds of cancers derived from patients with known outcomes permit one or more of DNA, RNA and protein assays to be performed on those arrays, to determine important prognostic markers, or markers predicting therapy outcome.

15 Tissue arrays may also be used to help assess optimal therapy for particular patients showing particular tumor marker profiles. For example, an array of tumors may be analyzed to determine which amplify and/or overexpress HER-2, such that the tumor type (or more specifically the subject from whom the tumor was taken) would be a good candidate for anti-HER-2 Herceptin immunotherapy. In another application, tissue arrays may be used to find novel targets for gene therapy. For example, cDNA hybridization patterns (such as on a DNA chip) may reveal differential gene regulation in a tumor of a particular tissue type (such as lung cancer), or a particular histological sub-type of the particular tumor (such as adenocarcinoma of the lung). Analysis of each at such gene candidates on a large tissue array containing hundreds of tumors would help determine which is the most promising target for developing diagnostic, prognostic or therapeutic approaches for cancer.

### EXAMPLE 1

#### Tissue Specimens

30 A total of 645 breast cancer specimens were used for construction of a breast cancer tumor tissue microarray. The samples included 372 fresh-frozen ethanol-fixed tumors, as well as 273 formalin-fixed breast cancers, normal tissues and fixation controls. The subset of frozen breast cancer samples was selected at random from the tumor bank of the institute of Pathology, University of Basel, which includes more than 1500 frozen breast cancers obtained by surgical resections during 1986-1997. Only the tumors from this tumor bank were used for molecular analyses. This subset was reviewed by a pathologist, who determined that the specimens included 259 ductal, 52 lobular, 9 medullary, 6 mucinous, 3 cribriform, 3 tubular, 2 papillary, 1 histiocytic, 1 clear cell, and 1 lipid rich carcinoma. There were also 15 ductal carcinomas in situ, 2

carcinosarcomas, 4 primary carcinomas that had received chemotherapy before surgery, 8 recurrent tumors and 6 metastases. Histological grading was only performed in invasive primary tumors that had not undergone previous chemotherapy. Of these tumors, 24% were grade 1, 40% grade 2, and 36% grade 3. The pT stage was pT1 in 29%, pT2 in 54%, pT3 in 9%, and pT4 in 8%. Axillary lymph nodes had been examined in 282 patients (45% pN0, 46% pN1, 9% pN2). All previously unfixed tumors were fixed in cold ethanol at +4 C overnight and then embedded in paraffin.

## EXAMPLE 2

### Immunohistochemistry

After formation of the array and sectioning of the donor block, standard indirect immunoperoxidase procedures were used for immunohistochemistry (ABC-Elite, Vector Laboratories). Monoclonal antibodies from DAKO (Glostrup, Denmark) were used for detection of p53 (DO-7, mouse, 1:200), erbB-2 (c-erbB-2, rabbit, 1:4000), and estrogen receptor (ER ID5, mouse, 1:400). A microwave pretreatment was performed for p53 (30 minutes at 90°C) and erbB-2 antigen (60 minutes at 90°C) retrieval. Diaminobenzidine was used as a chromogen. Tumors with known positivity were used as positive controls. The primary antibody was omitted for negative controls. Tumors were considered positive for ER or p53 if an unequivocal nuclear positivity was seen in at least 10% of tumor cells. The erbB-2 staining was subjectively graded into 3 groups: negative (no staining), weakly positive (weak membranous positivity), strongly positive (strong membranous positivity).

## EXAMPLE 3

### Fluorescent In Situ Hybridization (FISH)

Two-color FISH hybridizations were performed using Spectrum-Orange labeled cyclin D1, myc or erbB2 probes together with corresponding FITC labeled centromeric reference probes (Vysis). One-color FISH hybridizations were done with spectrum orange-labeled 20q13 minimal common region (Vysis, and see Tanner et al., *Cancer Res.* 54:4257-4260 (1994)), mybL2 and 17q23 probes (Barlund et al., *Genes Chrom. Cancer* 20:372-376 (1997)). Before hybridization, tumor array sections were deparaffinized, air dried and dehydrated in 70, 85 and 100 % ethanol followed by denaturation for 5 minutes at 74°C in 70 % formamide-2 X SSC solution. The hybridization mixture contained 30 ng of each of the probes and 15 µg of human Cot1 -DNA. After overnight hybridization at 37°C in a humidified chamber, slides were washed and counterstained with 0.2 µM DAPI in an antifade solution. FISH signals were scored with a Zeiss fluorescence microscope equipped with double-band pass filters for simultaneous visualization of FITC and Spectrum Orange signals. Over 10 FISH signals per cell or tight clusters of signals were considered as indicative of gene amplification.

**EXAMPLE 4****mRNA In Situ Hybridization**

For mRNA in situ hybridization, tumor array sections were deparaffinized and air dried before hybridization. Synthetic oligonucleotide probes directed against erbB2 mRNA (Genbank accession number X03363, nucleotides 350-396) was labeled at the 3'-end with <sup>33</sup>P-dATP using terminal deoxynucleotidyl transferase. Sections were hybridized in a humidified chamber at 42°C for 18 hours with 1 X 10<sup>7</sup> CPM/ml of the probe in 100 µL of hybridization mixture (50 % formamide, 10 % dextran sulfate, 1 % sarkosyl, 0.02 M sodium phosphate, pH 7.0, 4 X SSC, 1 X Denhardt's solution and 10 mg/ml ssDNA). After hybridization, sections were washed several times in 1 X SSC at 55°C to remove unbound probe, and briefly dehydrated. Sections were exposed for three days to phosphorimager screens to visualize ERBB2 mRNA expression. Negative control sections were treated with RNase prior to hybridization, which abolished all hybridization signals.

The present method enables high throughput analysis of hundreds of specimens per array. This technology therefore provides an order of magnitude increase in the number of specimens that can be analyzed, as compared to prior blocks where a few dozen individual formalin-fixed specimens are in a less defined or undefined configuration, and used for antibody testing. Further advantages of the present invention include negligible destruction of the original tissue blocks, and an optimized fixation protocol which expands the utility of this technique to visualization of DNA and RNA targets. The present method also permits improved procurement and distribution of human tumor tissues for research purposes. Entire archives of tens of thousands of existing formalin-fixed tissues from pathology laboratories can be placed in a few dozen high-density tissue microarrays to survey many kinds of tumor types, as well as different stages of tumor progression. The tumor array strategy also allows testing of dozens or even hundreds of potential prognostic or diagnostic molecular markers from the same set of tumors. Alternatively, the cylindrical tissue samples provide specimens that can be used to isolate DNA and RNA for molecular analysis.

**EXAMPLE 5****Tissue Microarrays For Gene Amplification Surveys In Many Different Tumor Types**

To facilitate rapid screening for molecular alterations in many different malignancies, a tissue microarray consisting of samples from 17 different tumor types, from 397 individual tumors, were arrayed in a single paraffin-block. Amplification of three oncogenes (CCND1, MYC, ERBB2) was analyzed in three Fluorescence in situ Hybridization (FISH) experiments from consecutive sections cut from the tissue microarray. Amplification of CCND1 was found in breast, lung, head

and neck, and bladder cancer as well as in melanoma. ERBB2 was amplified in bladder, breast, colon, stomach, testis, and the lung cancers. MYC was amplified in breast, colon, kidney, lung, ovary, bladder, head and neck, and endometrial cancer.

The microarray was constructed from a total of 417 tissue samples consisting of 397  
5 primary tumors from 17 different tumor types and 20 normal tissues which were snap-frozen and stored at -70°C. Specimens were fixed in cold ethanol (+4°C) for 16 hours and then embedded in paraffin. An H&E-stained section was made from each block to define representative tumor regions. Tissue cylinders with a diameter of 0.6 mm were then punched from tumor areas of each "donor" tissue block and brought into a recipient paraffin block using a custom-made precision instrument as  
10 described. Then 5 µm sections of the resulting multi-tumor tissue microarray block were transferred to glass slides using the paraffin sectioning aid system (adhesive coated slides, (PSA-CS4x), adhesive tape, UV-lamp; Instrumedics Inc., New Jersey) supporting the cohesion of 0.6 mm array elements.

The primary tumors consisted of 96 breast tumors (41 ductal, 28 lobular, 6 medullar, 5 mucinous, and 4 tubular carcinomas, 7 ductal carcinomas in situ (DCIS) and 5 phylloides tumors), 80  
15 carcinomas of the lung (31 squamous, 11 large cell, 2 small cell, 31 adeno, and 5 bronchioloalveolar carcinomas), 17 head and neck tumors (12 squamous cell carcinomas of the oral cavity and 5 of the larynx), 32 adenocarcinomas of the colon, 4 carcinoids (3 from the lung and one from the small intestine), 12 adenocarcinomas from the stomach, 28 clear cell renal cell carcinomas, 20 testicular tumors (10 seminomas and 10 terato-carcinomas), 37 transitional cell carcinomas of the urinary  
20 bladder (33 invasive (pT1-4) and 4 non-invasive tumors), 22 prostate cancers, 26 carcinomas of the ovary (12 serous, 12 endometrioid, and 2 mucinous tumors), 13 carcinomas from the endometrium, 3 carcinomas of the thyroid gland, 3 pheochromocytomas, and 4 melanomas. Normal tissue from breast, prostate, pancreas, small bowel, stomach, salivary gland, colon, and kidney were used as controls.

The tissue microarray sections were treated according to the Paraffin Pretreatment Reagent Kit protocol (Vysis, Illinois) before hybridization. FISH was performed with Spectrum Orange-labeled CCND1, ERBB2, and MYC probes. Spectrum Green-labeled centromeric probes CEP11 and CEP17 were used as a reference (Vysis, Illinois). Hybridization and post-hybridization washes were according to the 'LSI procedure' (Vysis, Illinois). Slides were then counterstained with  
30 125 ng/ml 4',6-diamino-2-phenylindole in antifade solution. FISH signals were scored with a Zeiss fluorescence microscope equipped with double-band pass filters for simultaneous visualization of Spectrum Green and Spectrum Orange signals (Vysis, Illinois). Amplification was defined as presence (in at least 5% of tumor cells) of either (a) more than 10 gene signals or tight clusters of at least 5 gene signals; or (b) more than 3 times as many gene signals than centromere signals of the  
35 respective chromosome.

Seventy-two amplifications were found in 968 successfully hybridized tumor samples, whereas none of the normal tissues showed amplification. Amplification usually involved almost all

tumor cells within an array element. CCND1 amplification was found in 6 of 16 head and neck carcinomas (38%), 14 of 62 breast carcinomas (23%), 1 of 6 DCIS (17%), 3 of 27 bladder cancers (11%), 7 of 76 carcinomas of the lung (9%), and 1 of 4 melanomas. MYC amplification was observed in 2 of 11 endometrial cancers (18%), 9 of 74 breast carcinomas (12%), 1 of 5 DCIS (20%), 1 of 17 head and neck cancers (6%), 1 of 22 tumors of the kidney (5%), 2 of 24 ovarian carcinomas (8%), 1 of 17 tumors of the testis (6%), 1 of 30 colon carcinomas (3%), 7 of 78 lung tumors (9%) and in 1 of 33 bladder tumors (3%). ERBB2 was amplified in 4 of 71 breast carcinomas (6%), 4 of 6 DCIS (67%), 2 of 11 stomach cancers (18%), 1 of 30 colon carcinomas (3%), 1 of 17 tumors of the testis (6%), and in 1 of 75 carcinomas of the lung (1%). Co-amplifications of all three genes were seen in two breast carcinomas. Co-amplifications of two genes were found in two breast carcinomas (CCND1/MYC and CCND1/ERBB2) and in one terato-carcinoma of the testis (MYC and ERBB2).

Consecutive sections cut from the block provide starting material for the in situ detection of multiple DNA, RNA or protein targets in many tissues at a time, in a massively parallel fashion. The tissue array technology permits increased capacity, automation, negligible damage to the original tissue blocks from which the specimens are taken, the precise positioning of tissue specimens, and the use of these tissues in different kinds of molecular analyses, besides immunostaining. It is possible to retrieve 10-20 punched samples (or more) from each donor block without significantly damaging it. This enables generation of multiple replicate array blocks, each with the identical coordinates, and the same specimens. The application of a precision instrument to deposit the samples in a predefined format also facilitates the development of automated image analysis strategies for the arrayed tumors. Depending on the thickness of the original tissue blocks, between 150 and 300 sections can be cut from each array block. This technology enables analyses of even small primary tumors, thereby preserving often unique and precious tumor specimens for a large number of analyses that may be of interest in future investigations.

The array data reported in this example agreed with the previous literature on the presence or absence of gene amplification in 73% of evaluations, although the number of samples per tumor type was too small for a comprehensive analysis of some tumor types in this pilot study. Previously described amplifications were not detected on the array in 9 of 25 tumor types from which less than 25 samples were examined. In contrast, when at least 25 cases were analyzed per tumor type, 92% of the known amplifications (11/12) were detected.

In this study, frozen tumor tissues were fixed in cold ethanol because this procedure allows the retention of good quality nucleic acids from fixed tissue samples. Even formalin-fixed tumor tissues, such as those obtained at autopsy, can be analyzed by FISH for DNA copy number alterations. However, the cold ethanol fixation is advantageous for FISH, because the samples require fewer pretreatments than samples fixed in 4% buffered formalin. Cold ethanol fixation may cause RNAs to degrade in paraffin blocks after only a few months of storage, hence it may not

be desired to fix a large series of precious tissues in cold ethanol, unless RNA inhibitors are added or blocks stored in a manner that prohibits this degradation.

#### EXAMPLE 6

##### 5 PDGFB FISH Experiments Using A Multi-Tumor Tissue Array

The multi-tumor tissue array of Example 5 was used in this experiment. A platelet derived growth factor  $\beta$  (PDGFB) probe was obtained from Vysis Inc. of Downers Grove, IL. The probe was obtained by PCR screening of a genomic large-insert library using two sequence tagged sites (STS) in the gene sequence as a target for developing PCR primers that were used in the PCR-based library screening. The hits obtained from genomic library screening were further verified by 10 their content of the STSs, as well as by hybridizing the probe to metaphase chromosomes using FISH. This resulted in a signal at the expected chromosomal location of PDGFB.

PCR/STS screening can be performed using a PCR primer set specific to the gene of interest, as described by Green & Olson, *PNAS USA* 87:1213-1217, 1990. Probes for FISH may 15 be generated from large-insert libraries (e.g. cosmids, P1 clones, BACs, PACs, etc.) using a PCR-based screening of arrayed and pooled large-insert libraries. Both Research Genetics (Huntsville, AL) and Genome Systems (St. Louis) perform such filter screening, and sell pools of DNA for performing library screening.

One method of isolating the P1 clone for PDGFB (pVYS309A) would be to screen 20 DNA pools of a human P1 library obtained from Genome Systems, Inc. Individual clones are identified by producing the expected DNA fragment size on gels after PCR. Bacterial cultures containing candidate PDGFB clones are purified by streaking on nutrient agar media for single colonies. Cultures from individual colonies are then grown and DNA isolated by standard techniques. The DNA is confirmed to contain the desired DNA sequence by PCR and gel 25 electrophoresis (STS confirmation). A sample of the DNA is labeled by nick-translation or random priming with SpectrumOrange dUTP (Vysis) and shown to hybridize to the expected region of chromosome 22q normal metaphase chromosomes by FISH.

PCR primers for PDGFB can be derived from the published sequence of the cDNA of this gene (GenBank Accession X02811). The preferred region of STS design is the 3' untranslated region of the cDNA. Several PCR primer sets for PDGFB are in public databases, e.g. amplimers 30 (PCR primer sets) PDGFB PCR1, PDGFB PCR2, PDGFB PCR3, stPDGFB.b, WI-8985, and can be found in the Genome Database (<http://gdbwww.gdb.org/gdb/gdbtop.html>). WI-8985 primer sets can also be found at the Whitehead Institute database (<http://www-genome.wi.mit.edu/>) and at the NIH Gene Map 98 database (<http://www.ncbi.nlm.nih.gov/genemap98/>).

35 FISH was done using standard protocols, as in Example 5, and hybridization of the probe to specimens of the tissue array was detected as in Example 5. Hybridization was detected in the following types of tumors:

- 29 -

	<b>TUMOR</b>	<b>Ratio Positive</b>	<b>Percent Positive</b>
	breast CA	2/70	2.9 %
	phylloides	0/4	
5	DCIS	0/7	
	lung	15/77	19 %
	colon	1/30	3.3%
	carcinoid	0/3	
	stomach	0/9	
10	renal cell	0/11	
	testis	1/16	6%
	TCC	10/32	31 %
	(bladder transitional cell carcinoma)		
	head/neck	0/17	
15	PCA	0/18	
	ovary	0/22	
	endometrium	2/8	25 %
	<b>total</b>	<b>22/324</b>	

20 The experiment of this Example provides the first evidence of previously unsuspected, high-level amplifications of PDGFB in specific types of malignancies, such as breast, lung, colon, testicular, endometrial and bladder cancer.

#### EXAMPLE 7

##### 25 Gene Amplifications During Prostate Cancer Progression

In this study, five different gene amplifications (AR, CMYC, ERBB2, Cyclin D1 and NMYC) were assayed by FISH from consecutive formalin fixed tissue microarray sections containing samples from more than 300 different prostate tumors. The objective was to obtain a comprehensive survey of gene amplifications in different stages of prostate cancer progression, including specimens from distant metastases. The tissue microarray contained minute samples from 371 specimens.

Formalin-fixed and paraffin-embedded tumor and control specimens were obtained from the archives of the Institutes for Pathology, University of Basel (Switzerland) and the Tampere University Hospital (Finland). The least differentiated tumor area was selected to be sampled for the tissue microarray. The minute specimens that were interpretable for at least one FISH probe included: I) transurethral resections from 32 patients with benign prostatic hyperplasia (BPH) which were used as controls; II) 223 primary tumors, including 64 cancers incidentally

detected in transurethral resections for BPH; stage T1a/b, 145 clinically localized cancers from radical prostatectomies, and 14 transurethral resections from patients with primary, locally extensive disease; III) 54 local recurrences after hormonal therapy failure including 31 transurethral resections from living patients and 23 specimens obtained from autopsies; IV) Sixty-two metastases  
5 collected at the autopsies from 47 patients who had undergone androgen deprivation by orchiectomy, and had subsequently died of end-stage metastatic prostate cancer. Metastatic tissue was sampled from pelvic lymph nodes (8), lung (21), liver (16), pleura (5), adrenal gland (5), kidney (2), mediastinal lymph nodes (1), peritoneum (1), stomach (1), and ureter (1). In 23 autopsies material was available from both the primary and from the metastatic site. More than  
10 one sample per tumor specimen was arrayed in 44 of the 339 cases. A tumor was considered amplified if at least one sample from the tumor exhibited gene amplification.

The array also included 48 pathologically representative samples which consistently failed in the analysis of sections with all FISH probes, and were therefore excluded from the analyses. Most of these were autopsy samples. The number of samples evaluable with the different  
15 probes was variable, because the hybridization efficiency of the probes was slightly different, some samples on the array were occasionally lost during the sectioning or FISH-procedure, and some tumors were only representative on the surface of the block, and the morphology changed as more sections were cut.

The prostate tissue microarray was constructed as previously described in Example 1,  
20 except with prostate instead of breast cancer specimens.

Two-color FISH to sections of the arrayed formalin-fixed samples was performed using Spectrum Orange-labeled AR, CMYC, ERBB2, and CyclinD1 (CCND1) probes with corresponding FITC-labeled centromeric probes (Vysis, Downer's Grove, Illinois). In addition, one-color FISH was done with a Spectrum Orange-labeled NMYC probe (Vysis). The  
25 hybridization was performed according to the manufacturer's instructions. To allow formalin-fixed tumors on the array to be reliably analyzed by FISH, the slides of the prostate microarray were first deparaffinized, acetylated in 0.2 N HCl, incubated in 1 M sodium thiocyanate solution at 80°C for 30 minutes and immersed in a protease solution (0.5mg/ml in 0.9% NaCl) (Vysis) for 10 minutes at 37°C. The slides were then post-fixed in 10% buffered formalin for 10 minutes, air  
30 dried, denatured for 5 minutes at 73°C in 70% formamide/2x SSC (SSC is 0.3M sodium chloride and 0.03M sodium citrate) solution and dehydrated in 70, 80, and 100% ethanol, followed by proteinase K (4µg/ml phosphate buffered saline) (GIBCOBRL, Life Technologies Inc., Rockville, Maryland) treatment for 7 minutes at 37°C. The slides were then dehydrated and hybridized.

The hybridization mixture contained 3µl of each of the probes and Cot1-DNA  
35 (1mg/ml; GIBCOBRL, Life Technologies Inc., Rockville, Maryland) in a hybridization mixture. After overnight hybridization at 37°C in a humid chamber, slides were washed, and counterstained with 0.2 µM DAPI. FISH signals were scored with a Zeiss fluorescence microscope equipped with



a double-band pass filter using x40-x100 objectives. The relative number of gene signals in relation to the centromeric signals was evaluated. Criteria for gene amplification were: at least 3 times more test probe signals than centromeric signals per cell in at least 10% of the tumor cells.

Test/control signal ratios in the range between 1 and 3 were regarded as low level gains, and were not scored as evidence of specific gene amplification. Amplification of NMYC without a reference probe was defined as at least 5 gene signals in at least 10% of the tumor cells.

High-quality hybridization signals with both centromeric and gene specific probes were obtained in 96% of the BPH samples for chromosome X/AR gene, 84% for chromosome 8/CMYC, 81% for chromosome 17/ERBB2, and 83% for chromosome 11/Cyclin D1. In the evaluable BPH samples, the average percentage of epithelial cells with two signals for autosomal probes was ~75%, with ~20% showing one signal and ~5% no signals. The percentage of cells with one or zero signals is believed to be attributable to the truncation of nuclei with sectioning. In the punched (single array element) samples of biopsy cancer specimens, AR, CMYC, ERBB2, and CCND1 FISH data could be obtained from 92%, 78%, 82%, and 86% of the cases, respectively. The success rate of FISH was lower in punches from autopsy tumors (44-58%). Amplifications were only scored to be present when the copy number of the test probe exceeded that of the chromosome-specific centromere reference probe by 3-fold in 10% or more of the tumor cells. This criterion was chosen, as low-level amplification is likely to be less relevant, and since locus-specific probes often display slightly higher copy numbers than centromeric probes, due to signal splitting or the presence of G2/M-phase cells.

FISH with the AR probe revealed amplification in 23.4% of the 47 evaluable hormone-refractory local recurrences. Amplification was seen equally often (22.0%) in 59 metastases of hormone-refractory tumors. The strong association between AR amplification and hormone-refractory prostate cancer is evident from the fact that only two of the 205 evaluable primary tumors (1%) and none of the 32 BPH controls showed any AR amplification. The two exceptions included a patient with locally advanced and metastatic prostate cancer, and another patient with clinically localized disease. Paired tumors from the primary site of the cancer and from a distant metastasis of 17 patients were successfully analyzed for AR amplification. In 11 of these patients, no AR amplification could be seen at either site. Of the six remaining patients, three patients showed amplification both in the local tumor mass, as well as in the distant metastases. In two cases amplification was only found in the sample from the primary site, whereas in another case only the distant metastasis showed amplification.

High-level CMYC amplifications were found in 5 of 47 evaluable metastatic deposits (10.6%), in 2 of the 47 local recurrences (4.3%, both metastatic cancers), but in none of the 168 evaluable primary cancers or 31 BPH controls. The comparison between different gene amplifications within the tumor cells defined by single punch-samples (array elements) showed that there was a significant association between AR and CMYC amplifications. CMYC was amplified

in 11.1% of 27 evaluable punch-samples with AR amplifications but only in 1.7% of 235 samples without AR amplifications ( $p=0.0041$ , contingency table analysis). AR was independently amplified in 24 samples, whereas only four samples had CMYC amplification, but no AR amplification.

5           On a tumor by tumor basis, there was a significant association between AR and CMYC amplifications. CMYC was amplified in 12.5% of 24 evaluable tumors with AR amplifications, but only in 1.8% of 219 tumors without AR amplifications ( $p=0.003$ , contingency table analysis). AR was independently amplified in 21 tumors, whereas only 4 tumors had CMYC amplification, but no AR amplification.

10           CCND1 amplifications were found in 2 (1.2%) of the 172 evaluable primary tumors, in 3 (7.9%) of 38 local recurrences, and in 2 (4.7%) of the 43 metastases. CCND1 amplification appeared independent from AR or CMYC amplification with 4/7 CCND1 amplified punched tumor samples not showing amplifications for any other genes tested. There were no ERBB2 amplifications among any of the 262 evaluable tumors or 31 BPH controls. Finally, a subset of the  
15           tumors was analyzed with the NMYC probe in a single color FISH analysis. Out of the 164 tumors available, none showed amplification, as defined by the lack of 5 or more signals per cell in > 10% of the tumor cells.

          For this study a tumor array was constructed that allowed investigation of the pattern of amplifications of multiple genes in samples representing the entire spectrum of prostate cancer  
20           progression, including distant metastases. The tumor array strategy facilitates standardized analysis of multiple genes in the same tumors, even in the same specific tumor sites using the same technology, with the same kind of probes, and similar interpretation criteria. In just five FISH experiments, 371 specimens were screened for five genes resulting in a total of over 1400 evaluable FISH results. The ability to achieve reliable detection of gene amplifications from formalin-fixed  
25           tissues substantially extends the range of possible applications for the tumor array technology.

          Many symptomatic prostate cancers become both hormone-refractory and metastatic, and it is difficult to distinguish between these two clinical features, or the molecular mechanisms that contribute to either of these processes. The results of the present example indicate that AR amplification is more closely associated with the development of hormone-refractory cell growth,  
30           whereas CMYC amplification is associated with metastatic progression. The most common gene amplification in prostate cancers is that of the AR gene, which is usually amplified independently of both CMYC and Cyclin D1. In this study, CMYC amplifications were more common in the distant metastases (11%) than in the locally recurrent tissues (4%; both from patients with end-stage metastatic cancers), whereas AR amplifications were equally common at both anatomical sites  
35           (22% and 23%, respectively). This suggests that AR is conferring an advantage for hormone-refractory growth, and not metastatic dissemination, whereas the reverse may be true for CMYC.

This Example indicates that the AR gene is the most frequent target, and often the first target, selected for amplification during prostate cancer progression. Second, in contrast to AR, amplifications of the CMYC oncogene appear to be primarily associated with metastatic dissemination. Finally, prostate cancers occasionally also amplify the Cyclin D1 gene, whereas  
5 ERBB2 and NMYC amplifications are unlikely to play a significant role at any stage of the progression of prostate cancer.

## EXAMPLE 8

**Rapid Screening For Prognostic Markers In Renal Cell Carcinomas (RCC) By Combining  
cDNA-Array And Tumor-Array Technologies**

5 This example first uses cDNA arrays to identify genes that play a role in renal cell carcinoma (RCC), and subsequently analyzes emerging candidate genes on a tumor array for their potential clinical significance. The results show that the combination of nucleic acid arrays and tumor arrays is a powerful approach to rapidly identify and further evaluate genes that play a role in RCC biology.

10 cDNA was synthesized and radioactively labeled using 50  $\mu$ g of total RNA from normal kidney (Invitrogen) and a renal cancer cell line (CRL-1933) (ATCC, VA, USA) according to standardized protocols (Research Genetics; Huntsville, AL). Release 1 of the human GeneFilters from Research Genetics was used for differential expression screening. A single membrane contained 5184 spots each representing 5 ng of cDNA of known genes or expressed sequence tags (EST's). After separate hybridization the two cDNA array filters (Research Genetics) were  
15 exposed to a high resolution screen (Packard) for three days. The gene expression pattern of 5184 genes in normal tissue and the tumor cell line was analyzed and compared on a phosphor imager (Cyclone, Packard). To define genes/EST's as under- or overexpressed, both an at least tenfold expression difference between normal tissue and the cell line using the Pathfinder software (Research Genetics; Huntsville, AL) and visual confirmation of an unequivocal difference in the  
20 staining intensity on filters was requested.

For the construction of the renal tumor microarray block, a collection of 615 renal tumors after nephrectomy was screened for availability of representative paraffin-embedded tissue specimens. Tumor specimens from 532 renal tumors and tissue from 6 normal kidneys were selected for the tumor array. The tumors were staged according to TNM classification, graded  
25 according to Thoenes (*Pathol. Res. Pract.* 181:125-143, 1986) and histologically subtyped according to the recommendations of the UICC (Bostwick et al., *Cancer* 80:973-1001, 1997) by one pathologist. Core-tissue-biopsies (diameter 0.6 mm) were taken from selected morphologically representative regions of individual paraffin-embedded renal tumors (donor blocks) and precisely arrayed into a new recipient paraffin block (45mm x 20mm) using a custom-built instrument. Then  
30 5  $\mu$ m sections of the resulting tumor tissue micro array block were transferred to glass slides using the paraffin sectioning aid system (adhesive coated slides, (PSA-CS4x), adhesive tape, UV-lamp; Instrumedics Inc., New Jersey) supporting the cohesion of 0.6 mm array elements.

Standard indirect immunoperoxidase procedures were used for immunohistochemistry (ABC-Elite, Vectra Laboratories) as described, for example in Moch et al., *Hum. Pathol.* 28:1255-  
35 1259, 1997. A monoclonal antibody was employed for vimentin detection (anti-vimentin; Boehringer Mannheim, Germany, 1:160). Tumors were considered positive for vimentin, if an unequivocal cytoplasmic positivity was seen in tumor cells. Vimentin positivity in endothelial cells

served as an internal control. The vimentin positivity in epithelial cells was defined as negative (no staining) or positive (any cytoplasmic staining).

Contingency table analysis was used to analyze the relationship between vimentin expression, grade, stage, and tumor type. Overall survival was defined as the time between  
5 nephrectomy and patient death. Survival rates were plotted using the Kaplan-Meier method. Survival differences between the groups were determined with the log-rank test. A Cox proportional hazard analysis was used to test for independent prognostic information.

Two cDNA array membranes were hybridized with radioactive-labeled cDNA from normal kidney and tumor cell line CRL-1933. The experiment resulted in 89 differentially  
10 expressed genes/EST's. An overexpression in CRL-1933 was found for 38 sequences, including 26 named genes and 12 EST's while 51 sequences (25 named genes, 26 EST's) were underexpressed in the cell line. The sequence of one of the upregulated genes in the cell line was identical to vimentin.

The presence of epithelial tumor cells was tested for every tissue cylinder using an  
15 H&E-stained slide. Vimentin expression could be evaluated on the tissue cylinders in 483 tumors and all 6 normal kidney tissues. Vimentin expression was frequent in clear-cell (51%) and papillary RCC (61%) but rare in 23 chromophobe RCC (4%). Only 2 of 17 oncocytomas showed a weak vimentin expression (12%). Normal renal tubules did not express vimentin. The association between vimentin expression and histological grade and tumor stage was only evaluated for clear  
20 cell RCC. Vimentin expression was more frequent in grade II (44%) and grade III (42%) than in grade I (13%) RCC ( $p < 0.0001$ ). Vimentin expression was more common in higher tumor stages (60% in stage pT1/2 versus 40% in stage pT3/4), but this difference was not significant ( $p = 0.09$ ).

There was a mean follow-up of  $52.9 \pm 51.4$  months (median, 37, minimum 0.1,  
25 maximum 241 months). Poor overall survival was strongly related to high histologic grade ( $p < 0.0001$ ) and high tumor stage ( $p < 0.0001$ ). The association between patient prognosis and vimentin expression was evaluated for patients with clear cell RCC. Vimentin expression was strongly associated with short overall survival ( $p = 0.007$ ). Proportional Hazards analysis with the variables tumor stage, histological grade and vimentin expression indicates that vimentin expression  
30 was an independent predictor of prognosis, the relative risk being 1.6 ( $p = 0.01$ ) in clear cell RCC.

The results of this example show that the combination of cDNA and tumor arrays is a powerful approach for identification and further evaluation of genes playing a role in human malignancies. This example illustrates that cDNA arrays may be used to search for genes that are differentially expressed in tumor cells (such as kidney cancer) as compared to normal tissue (kidney  
35 tissue in this example). Evaluation of all candidate genes emerging from a cDNA experiment on a representative set of uncultured primary tumors would take years if traditional methods of molecular pathology were used. However the tumor microarray technology markedly facilitates

such studies. Tissue arrays allow the simultaneous in situ analysis of hundreds of tumors on the DNA, RNA and protein level, and even permits correlation with clinical follow up data.

This high throughput analysis allowed marked differences in the vimentin expression between renal tumor subtypes to be illustrated. Vimentin was frequently detected in papillary and clear cell RCC, but rarely in oncocytoma and chromophobe RCC. Given the high rate of vimentin positivity in clear cell RCC detected in this example, the presence of vimentin expression may be used as a diagnostic feature to distinguish a diagnosis of clear cell RCC from chromophobe RCC.

This example further illustrates that tumor tissue arrays can facilitate the translation of findings from basic research into clinical applications. The speed of analysis permits a multi-step strategy. First, molecular markers or genes of interest are assessed on a master multi-tumor-array containing samples of many (or all) possible human tumor type. In a second step, all tumor types that have shown alterations in the initial experiment are then further examined on tumor type-specific arrays (for example bladder cancer) containing much higher numbers of tumors of the same tissue type, with clinical follow up information on survival or response to specific therapies. In a third step the analysis of conventional (large) diagnostic histologic and cytologic specimens is then restricted to those markers for which promising data emerged during the initial array based analyses. For example, vimentin expression can now be studied on larger tissue specimens to confirm its prognostic significance in clear cell RCC. If the array data are confirmed, vimentin immunohistochemistry may then be included in prospective studies investigating prognostic markers in RCC.

## EXAMPLE 9

### DNA Array Technology

Instead of using a single probe to test for a specific sequence on the sample DNA, a Gene or DNA chip incorporates many different "probes." Although a "probe" usually refers to what is being labeled and hybridized to a target, in this situation the probes are attached to a substrate. Many copies of a single type of probe are bound to the chip surface in a small spot which may be, for example, approximately 0.1 mm or less in diameter. The probe may be of many types including DNA, RNA, cDNA or oligonucleotide. In variations of the technology, specific proteins, polypeptides or immunoglobulins or other natural or synthetic molecules may be used as a target for analyzing DNA, RNA, protein or other constituents of cells, tissues or other biological specimens. Many spots, each containing a different molecular target, are then arrayed in the shape of a grid. The surface for arraying may be a glass, or other solid material, or a filter paper or other related substance useful for attaching biomolecules. When interrogated with labeled sample, the chip indicates the presence or absence of many different sequences or molecules in that specimen. For example, a labeled cDNA isolated from a tissue can be applied on a DNA chip to assay for expression of many different genes at a time.

The power of these chips resides not only in the number of different sequences or other biomolecules that can be probed simultaneously, as explained below for nucleic acid chips. In the analysis of nucleic acids, a relatively small amount of sample nucleic acid is required for such an analysis (typically less than a millionth of a gram of nucleic acid). The binding of nucleic acid to the chip can be visualized by first labeling the sample nucleic acid with fluorescent molecules or a radioactive label. The emitted fluorescent light or radioactivity can be detected by very sensitive cameras, confocal scanners, image analysis devices, radioactive film or a Phosphorimager, which capture the signals (such as the color image) from the chip. A computer with image analysis software detects this image, and analyzes the intensity of the signal for each probe location in the array. Detection of differential gene expression with a radioactive cDNA array was already described in Example 8. Usually, signals from a test array are compared with a reference (such as a normal sample).

DNA chips may vary significantly in their structure, composition, and intended functionality, but a common feature is usually the small size of the probe array, typically on the order of a square centimeter or less. Such an area is large enough to contain over 2,500 individual probe spots, if each spot has a diameter of 0.1 mm and spots are separated by 0.1 mm from each other. A two-fold reduction in spot diameter and separation can allow for 10,000 such spots in the same array, and an additional halving of these dimensions would allow for 40,000 spots. Using microfabrication technologies, such as photolithography, pioneered by the computer industry, spot sizes of less than 0.01 mm are feasible, potentially providing for over a quarter of a million different probe sites.

Targets on the array may be made of oligomers or longer fragments of DNA. Oligomers, containing between 8 and 20 nucleotides, can be synthesized readily by chemical methods. Photolithographic techniques allow the synthesis of hundreds of thousands of different types of oligomers to be separated into individual spots on a single chip, in a process referred to as in situ synthesis. Long pieces of DNA, on the other hand, contain up to several thousand nucleotides, and can not be synthesized through chemical methods. Instead, they are excised from the human genome and inserted into bacterial cells through genetic engineering techniques. These cells, or clones, serve as a convenient source for these DNAs, which can be produced in large quantities by fermentation. After extraction and appropriate chemical preparation the DNA from each clone is deposited onto the chip by a robot, which is equipped either with very fine syringes or with an ink-jet system.

The targets on the DNA chip interact with the DNA that is being analyzed (the target DNA) by hybridizing. The specificity of this process (the accuracy with which the sample nucleic acid sequences will bind to their complementary arrayed target sequences) is mainly a function of the length of the probe. For short oligonucleotide probes, the conditions can be chosen such that a single point mutation (the change of a single nucleotide in a gene) can be detected. That may

require as many as 65,536 or even more different oligonucleotide probes on a single chip to unambiguously deduce the sequence of even a relatively small DNA sequence. This process, called sequencing by hybridization (SbH), generates very complex hybridization patterns that are interpreted by image analysis computer software. In addition, the sequence to be analyzed is preferably short, and it must be isolated and amplified from the rest of the genome through a technique called Polymerase Chain Reaction (PCR), before it is applied to the chip for sequence analysis

In Comparative Genomic Hybridization (CGH), DNA from a sample tissue, such as a tumor, is compared to normal human DNA. In a particular example of CGH performed by Vysis, Inc., this is accomplished by labeling the sample DNA with a fluorescent dye, and the reference ("normal") DNA with a fluorescent dye of a different color. Both DNAs are then mixed in equal amounts and hybridized to a DNA chip. The Vysis chip or genosensor, contains an array of large insert DNA clones, each comprising approximately 100,000 nucleotides of human DNA sequence. After hybridization, a multi-color imaging system determines the ratio of colors (for example green to red fluorescence) for each of the probe spots in the array. If there is no difference between the sample DNA and the normal DNA, then all spots should have an equal mixture of red and green fluorescence, resulting in a yellow color. A shift toward green or red for a given spot would indicate that either more green or more red labeled DNA was bound to the chip by that probe sequence. This color shift indicates a difference between the sample and the reference DNA for that particular region on the human genome, pointing either toward amplification or deletion of a specific sequence or gene contained in the clones positioned in the array. Examples of genetic changes that can be detected include amplifications of genes in cancer, or characteristic deletions in genetic syndromes, such as Cri du chat.

Since each genetic region to be analyzed needs to be represented on the chip in only 1 or few replicate spots, the genosensor can be designed to scan the total human genome for large deletions or duplications in a single assay. For example, an array of just 3000 different clones evenly spaced along the human genome would provide a level of resolution that is at least 10 times better than what can be achieved with metaphase hybridization, at a much lower cost and in much less time. Specialty chips can be tailored to the analysis of certain cancers or disease syndromes, and can also provide physicians with much more information on routine clinical analysis than currently can be obtained even by the most sophisticated research laboratories.

The color ratio analysis of the genosensor CGH (gCGH) assay has the advantage that absolute quantitation of the amount of a specific sequence in the sample DNA is not necessary. Instead, only the relative amount compared to the reference (normal) DNA is measured with relatively high accuracy. This approach is equally useful for a third kind of chip technology, referred to as "Expression Chips." These chips contain arrays of probe spots which are specific for different genes in the human genome. They do not measure the presence or absence of a



mutation in the DNA directly, but rather determine the amount of message that is produced from a given gene. The message, or mRNA, is an intermediary molecule in the process by which the genetic information encoded in the DNA is translated into protein. The process by which mRNA amounts are measured involves an enzymatic step which converts the unstable mRNA into cDNA, and simultaneously incorporates a fluorescent label. cDNA from a sample tissue is labeled in one color and cDNA from a normal tissue is labeled with a different color. After comparative hybridization to the chip, a color ratio analysis of each probe spot reveals the relative amounts of that specific mRNA in the sample tissue compared to normal tissue. Expression chips measure the relative expression of each gene for which there is a probe spot on the chip.

There are approximately 100,000 different genes in the human genome, and it is expected that all of them will be known within a few years. Since chips with thousands of different probe spots can be made, the relative expression of each gene can be determined in a single assay. This has significant implications for disease diagnosis and therapy. Expression chips may be used to test the effect of drugs on the expression of a limited number of genes in tissue culture cells, by comparing mRNA from drug treated cells to that of untreated cells. The ability to measure the effect on the regulation of all genes will allow a much more rapid and precise drug design, since the potency and potential side effects of drugs can be tested early on in development. Moreover, the rapid increase in understanding of the regulatory switches that determine tissue differentiation will allow for the design of drugs that can initiate or modify these processes. Findings about differential expression in CGH can be further analyzed in tissue arrays, in which expression of mRNA can also be determined.

In one particular embodiment of CGH, a DNA chip or genosensor (gCGH), such as an AmpliOnc™ chip from Vysis, contains an array of P1, BAC or PAC clones, each with an insert of human genomic DNA. The size of these inserts ranges from 80 to 150 Kilobases, and they are spaced along the human genome to improve the resolution of this technique. Since the hybridization probe mixture contains only on the order of 200 ng of total human DNA from each of the test and reference tissue, the total number of available probes for each arrayed target clone is relatively low, placing higher demands on the sensitivity of this system than what is needed for regular fluorescent in situ hybridization techniques. These demands have been met with the development of improved chip surfaces, attachment chemistry, and imaging systems. The combination of such features can provide a sensitivity of  $< 10^8$  fluorophors/cm<sup>2</sup>, which is achieved through highly efficient background reduction.

Autofluorescence emanating from the chip surface may be reduced by coating the glass chip with chromium, as disclosed in U.S. Patent Application No. 09/085,625. This highly reflective surface provides enhanced signal collection efficiency, and its hydrophobic nature reduces non-specific binding of probes. Efficient reading of CGH chips is achieved with a sensitive, high speed, compact, and easy to use multicolor fluorescence imaging system, such as that described in

U.S. Patent Application No. 09/049,748. Its non-epifluorescent excitation geometry eliminates autofluorescence from the collection optics, and collects only fluorescent light from the chip surface. A xenon arc lamp serves as a safe and long-lasting light source, providing even illumination over a wide range of wavelengths. This allows for the use of many different fluorophores, limited only by the choice of excitation and emission filters. Fluorescent images are acquired from a 14 mm x 9 mm sample area by a cooled CCD camera without scanning or magnification, and even the need for routine focusing has been eliminated. The images are analyzed by software, which interrogates each individual pixel to calculate the ratio of sample to reference probe that are hybridized to each target spot. An appropriate statistical analysis reveals the relative concentration of each target specific sequence in the probe mixture.

This system may be used for expression analysis or genomic applications, such as an analysis of genetic changes in cancer. For this purpose a microarray was developed for the specific analysis of all genetic regions that have been reported so far to be associated with tumor formation through amplification at the genome level. The AmpliOnc™ chip contains 33 targets (mostly known oncogenes), each replicated 5 times. A schematic representation of such a chip (and 31 of the targets) is shown in FIG. 24.

#### EXAMPLE 10

##### Combination of Microarrays to Detect Amplification of FGFR2 Gene in Sum-52 Breast Cancer Cell Line

This Example demonstrates how target genes for chromosomal gains seen by comparative genomic hybridization (CGH) can be rapidly identified and studied for their clinical relevance using a combination of novel, high-throughput microarray strategies. CGH to metaphase spreads (FIG. 25, chromosomal CGH) showed high-level DNA amplifications at chromosomal regions 7q31, 8p11-p12 and 10q25 in the Sum-52 breast cancer cell line. Genomic DNA from the Sum-52 cell line was then hybridized to a novel CGH microarray (FIG. 25, genosensor CGH, Vysis, Downers Grove, IL), which enabled simultaneous screening of copy number at 31 loci containing known or suspected oncogenes (the loci are shown in FIG. 24). This gCGH analysis implicated specific, high-level amplifications of the MET (at 7q31) and FGFR2 (at 10q25) genes, as well as low level amplification of the FGFR1 gene (at 8p11-p12), indicating the involvement of these three genes in the amplicons seen by conventional CGH analysis. A large-scale expression survey of the same cell line using a cDNA microarray (Clontech Inc.) provided additional information. The FGFR2 gene was the most abundantly overexpressed transcript in the SUM-52 cells implicating this gene as the likely amplification target gene at 10q25. Overexpression of FGFR2 was confirmed by Northern analysis, and amplification by fluorescence in situ hybridization (FISH). Finally, FISH to a tissue microarray consisting of 145 primary breast cancers (FIG. 26) showed the in vivo amplification of the FGFR2 gene in 4.5% of the cases.

These three microarray experiments can be accomplished in a few days, and illustrate how the combination of microarray-based screening techniques is very powerful for the rapid identification of target genes for chromosomal rearrangements, as well as for the evaluation of the prevalence of such alterations in large numbers of primary tumors. This power is conferred by the ability to screen many genes against one tumor, using DNA array technologies (such as cDNA chips or CGH), to find a gene of interest, in combination with the ability to screen many tumors against the gene of interest using the tissue microarray technology. FIG. 27 illustrates that the DNA chip can use multiple clones (for example more than 100 clones) to screen a single tumor or other cell, while the complementary tissue microarray technology can use a single probe to screen multiple (for example more than 100) tumor or other tissue specimens (of either the same or different tissue types).

#### EXAMPLE 11

##### **Tissue Arrays To Determine Frequency And Distribution Of Gene Expression and Copy Number Changes During Cancer Progression**

Tissue arrays may be used to follow-up genes and targets discovered from, for example, high-throughput genomics, such as DNA sequencing, DNA microarrays, or SAGE (Serial Analysis of Gene Expression) (Velculescu et al., Science, 270:484-487, 1995). Comparative analysis of gene expression patterns with cDNA array technology (Skena 1995 and 1996) provides a high-throughput tool for screening expressional changes for better understanding molecular mechanisms responsible for tumor progression as well as aiming for discovery of new prognostic markers and potential therapeutic targets. Tissue arrays provide accurate frequency and distribution information concerning such genes in both pathological and normal physiological conditions.

An example is the use of a prostate tumor array to determine that IGFBP2 (Insulin Growth factor binding protein 2) is a marker associated with progression of human prostate cancer. To elucidate mechanisms underlying the development and progression of hormone refractory prostate cancer, gene expression profiles were compared for four independent CWR22R hormone refractory xenografts to androgen dependent CWR22 primary xenograft. The CWR22 xenograft model of human prostate cancer was established by transplantation of human prostate tumor cells into the nude mouse [Pretlow, *J. Natl. Cancer Inst.* 3:394-398,1993]. This parental tumor xenograft is characterized by secretion of prostate specific antigen (PSA) and with rapid reduction of tumor size in response to the hormone-withdrawal therapy. Approximately half of the treated animals will develop recurrent tumors from a few weeks to several months. These recurrent tumors are resistant to further hormonal treatments when transferred to the new host. They also are characterized by a more aggressive phenotype than parental CWR22 tumors, and eventually lead to

death of the animal. This experimental model mimics the course of prostate cancer progression in human patients.

Comparison of the expression levels of 588 known genes during the progression of the CWR22 prostate cancer in mice was performed with the cDNA microarray technology. RNA was prepared from CWR22 xenografts as described earlier with minor modifications [Chirgwin, 1979]. The mRNA was purified using oligo(dT) selection with DynaBeads (Dynal) according to manufacturers instructions. The cDNA array hybridizations were performed on AtlasII cDNA arrays (Clontech) according to manufacturers instructions. The cDNA probes were synthesized using 2 µg of polyA<sup>+</sup> RNA and labeled with 32P a dCTP.

The gene expression pattern in a hormone-sensitive CWR22 xenograft was compared with that of a hormone-refractory CWR22R xenograft. Expressional changes of several genes, which have previously been shown to be involved in prostate cancer pathogenesis were detected. In addition multiple genes were identified with no previous connection to prostate cancer, nor had they been known to be regulated by androgens. One of the most consistently upregulated genes, Insulin-like Growth Factor Binding Protein 2 (IGFBP-2), was chosen for further study. The tissue microarray technology was used to validate that the IGFBP2 expression changes also take place in vivo, during the progression of prostate cancer in patients undergoing hormonal therapy.

Formalin-fixed and paraffin-embedded samples from a total of 142 prostate cancers were used for construction of the prostate cancer tissue microarray. The tumors included 188 non-hormone refractory primary prostate cancers, 54 transurethral resection specimens of locally recurrent hormone-refractory cancers operated during 1976-1997, and 27 transurethral resections for BPH as benign controls. The subset of the primary non-hormone refractory tumors and benign controls was selected from the archives of the Institute for Pathology, University of Basel, (Switzerland), and the subset of hormone-refractory tumors from the University of Tampere (Finland). The group of primary non-hormone refractory prostate cancers consisted of 50 incidentally detected tumors in transurethral resections for presumed BPH (pT1a/b), and 138 radical prostatectomy specimens of patients with clinically localized disease. The specimens were fixed in 4 per cent phosphate-buffered formalin. The sections were processed into paraffin and slides were cut at 5 µm and stained with haematoxylin and eosin (H & E). All sections were reviewed by one pathologist, and the most representative (usually the least differentiated) tumor area was delineated on the slide. The tissue microarray technology was used as previously described to construct the tissue array.

Standard indirect immunoperoxidase procedures were used for immunohistochemistry (ABC-Elite, Vector Laboratories). The goat polyclonal antibody IGFBP-2, C-18 (1:x, Santa Cruz Biotechnology, Inc., California) was used for detection of IGFBP-2 after a microwave pretreatment. The reaction was visualized by diaminobenzidine as a chromogen. Positive controls for IGFBP-2 consisted of normal renal cortex. The primary antibody was omitted for negative

controls. The intensity of the cytoplasmic IGFBP-2 staining was estimated and stratified into 4 groups (negative, weak, intermediate, and strong staining).

There was a strong relationship between IGFBP-2 staining and progression of cancer to a hormone refractory disease with an increasing frequency of high-level staining. Strong IGFBP-2 staining was present in none of the normal glands, in 30% of the non-hormone-refractory primary tumors but in 96% of the recurrent, hormone-refractory prostate cancers ( $p=0.0001$ ). Hence this example provides another case in which a high-throughput expression survey by cDNA array hybridization indicated a specific gene, which may be involved in disease progression. This hypothesis could be directly validated using the tissue array technology. The results have identified IGFBP2 to be used as a target for developing diagnostic, prognostic or therapeutic approaches to the management of patients with advanced prostate cancer.

#### EXAMPLE 12

##### Platelet Derived Growth Factor B In Breast Cancer

The breast cancer SKBR3 cell line was screened with the AmpliOnc DNA array, and Platelet Derived Growth Factor B (PDGF B) was identified as being amplified. Using this information, a PDGF B probe was made using a clone identical to the PDGF B clone used in the AmpliOnc array. This probe was used to screen a breast cancer tumor array. It was found that only 2% of all the breast cancers screened were amplified for PDGF B. A multi-tumor array (described in Example 6) was then probed using this probe. This revealed that, unexpectedly, the PDGF B gene was amplified in a large percentage of lung and bladder cancers. Thus, using the invention, a novel marker of diagnostic importance in these other types of tumors was identified.

#### EXAMPLE 13

##### Herceptin Treatment

Tissue arrays may be used to screen large numbers of tumor tissue samples to determine which tumors would be susceptible to a particular treatment. For example, a breast cancer array may be screened for expression of the HER-2 gene (also called ERBB2 in Example 1), as explained in Example 1. Tumors that over-express and/or amplify the HER-2 gene may be good candidates for treatment with herceptin, which is an antibody that inhibits the expression of HER-2. Screening of the multi-tumor tissue array with the HER-2 antibodies or a DNA probe would provide information about cancers other than breast cancer that could be successfully treated with the Herceptin therapy.

**EXAMPLE 14****Correlating Prognosis And Survival With Markers**

Tumor tissue arrays constructed from tumors taken from patients for whom history and outcome is known may be used to assess markers with prognostic relevance.

- 5 This example illustrates that prognostic markers in urinary bladder cancer can be evaluated using tumor tissue arrays, in spite of any intratumor heterogeneity.

An array of 315 bladder tumors was analyzed for nuclear p53 accumulation by immunohistochemistry. The p53 analysis was done twice; once on conventional large histological sections taken from entire tumor blocks and once on a section from a tumor  
10 array containing one sample from each tumor. The tumor series consisted of 127 pTa, 81 pT1, and 128 pT2-4 bladder carcinomas with clinical follow up information (tumor specific survival).

One block per tumor was analyzed. One section was taken from each block for immunohistochemical analysis. Then a tissue array was constructed by taking one  
15 "punch biopsy" from each block and bringing it in an empty recipient block. Sections 4  $\mu$ m thick were taken from primary tumor blocks and from the array block. The monoclonal antibody DO-7 (DAKO, 1:1000) was applied for immunostaining using standard procedures.

On large sections a tumor was considered positive if a moderate or strong  
20 nuclear p53 staining was seen in at least 20% of tumor cells, at least in an area of the tumor. On array sections a tumor was considered positive if a moderate or strong nuclear p53 staining was seen in at least 20% of arrayed tumor cells. Weak nuclear and any cytoplasmic p53 staining was disregarded.

A Chi-square test was used to compare the p53 results between array and  
25 large sections. Survival curves were plotted according to Kaplan-Meier. A log rank test was applied to examine the relationship between p53 positivity and tumor specific survival. Surviving patients were censored at the time of their last clinical control. Patients dying from other causes than their bladder tumor were censored at the time of death.

Results showed that p53 could be analyzed on 315 arrayed tumor samples (21  
30 samples were absent on the p53 stained array section). On conventional sections, p53 immunostaining was positive in 105 of these 315 tumors which were also present on the array. p53 positivity as detected on conventional "large" sections was significantly linked to poor prognosis (Figure 1A,  $p < 0.0001$ ). Only 69 of these 105 tumors (66%) that were p53 positive on large sections were also positive on arrayed tumor samples, while 36  
35 (34%) remained negative probably because of tumor heterogeneity. Nevertheless, there was a strong association between p53 immunostaining results on arrays and on large

sections ( $p < 0.0001$ ) and p53 positivity on arrays was still significantly linked to poor prognosis (Figure 1B,  $p = 0.0064$ ).

The specific number of biopsies from each tumor that are preferably obtained to reproduce 90%, 95% or 100% of the information obtained from the whole-section analysis will make it possible to determine how many "punches" with the tissue arrays are required to extract clinically significant information from the tissue array experiments. This optimal number may vary depending on the tumor type and the specific biological target that will be analyzed.

10

### EXAMPLE 15

#### Novel Gene Targets

Tissue arrays may be used to find novel targets for cancer therapies. Hundreds of different genes may be differentially regulated in a given cancer (based on cDNA, e.g. microarray, hybridizations, or other high-throughput expression screening methods such as sequencing or SAGE). Analysis of each gene candidate on a large tissue array can help determine which is the most promising target for development of novel drugs, inhibitors, etc. For instance, a tumor array containing thousands of diverse tumor samples may be screened with a probe for an oncogene, or a gene coding for a novel signal transduction molecule. Such a probe may bind to one or a number of different tumor types. If a probe reveals that a particular gene is overexpressed and or amplified in many tumors, then that gene may be an important target, playing a key role in many tumors of one histological type or in different tumor types. Therapies directed to interfering with the expression of that gene or with the function of the gene product may be promising novel cancer drugs. In particular, the tissue arrays can help to prioritize the selection of targets for drug development.

25

### EXAMPLE 16

#### Tissue Array Followed by DNA Array

Although many of the foregoing examples have described the DNA array being used prior to the tissue array, the present invention includes use of these arrays in either order, or in combination with other analytic techniques. Hence genes of interest noted when probing multiple tumor samples with a single probe during tissue array analysis can subsequently be selected to be placed on a DNA array, using a unique sequence from the gene of interest as one of the probes attached to the array substrate. For example, one could tailor a DNA chip that has most diagnostic, prognostic or therapeutic relevance based on information from the microarray experiment.

35

Some possible interrelationship of cDNA arrays, CGH arrays, and tissue arrays is shown in FIG. 28. As illustrated in that Figure, the various assays can be performed in any order, or in any combination.

**EXAMPLE 17****Cell line arrays**

Cultured cells or cells isolated from non-solid tissues or tumors (such as blood samples, bone marrow biopsies, cytological specimens obtained by needle aspiration biopsies etc.) can also be analyzed with the tissue array techniques. This is an important extension of the tissue array technology to the analysis of individual cells, or populations of cells obtained either directly from people or animals or after various incubations of cell culture experiments have been performed in vitro (such as a specific hormonal or chemotherapeutic test often performed on a microtiter tray format for pharmaceutical drug screening). In the analysis of malignancies, this would enable analysis of leukemias and lymphoma tissues or other liquid tumor types following the same strategies described above for solid tumors. Using this approach, cancer cell lines obtained from the American Type Culture Collection (Rockville, MD) were used. Cells were trypsinized and the cell suspensions were spun down with a centrifuge at 1200 G. The cell pellet was fixed with alcohol-based and formaldehyde fixatives, and the fixed cell pellet was embedded in paraffin following the routine protocols used in pathology laboratories. The fixed and embedded cell suspensions can then be used as starting material for the development of cell arrays, using the same procedure as described previously for the fixed and embedded tissue specimens. It is anticipated that up to or at least 1000 different cell populations can be arrayed in a single standard-size paraffin block.

Very small punch sizes (for example less than 0.5 mm) can be used for creating arrays from homogenous cultured cells. This allows high density arrays to be constructed. For example, approximately 2000 different cell populations can be placed in a single 40 mm x 25 mm paraffin block.

The method of analyzing tissue in accordance with the present invention can take many different forms, other than those specifically disclosed in the above examples. The tissue specimens need not be abnormal, but can be normal tissue for analyzing the function and tissue distribution of a specific gene, protein, or other biomarker (where a biomarker is a biological characteristic that is informative about a biological property of the specimen). The normal tissue could include embryonal tissues, or tissues from genetically modified organisms, such as a transgenic mouse.

The array technology can also be used to analyze diseases that do not have a genetic basis. For example, the gene or protein expression patterns could be profiled that are likely to have importance for the pathogenesis or diagnosis of the disease. The tissue specimens need not be limited to solid tumors, but can also be used with cell lines, hematological or other liquid tumors, cytological specimens, or isolated cells.



Cells of humans or other animals may be used in a suspension, as may cells of yeast or bacteria. Alternatively, cells in suspension may be spun down in a centrifuge to provide a solid or semi-solid pellet, fixed, and then placed in the array, much like a tissue specimen. Liquid cellular suspensions may be placed with a pipette into a matrix (for example depressions in a slide surface) and then can also be analyzed in the same manner as the tissue array already described. The tissue arrays can also be used in cell line experiments, such as high throughput chemotherapeutic screening of cells grown in microtiter plates. The cells from each well are treated with a different drug or a different concentration of the drug, and are then recovered and inserted into a cell line microarray to analyze their functional characteristics, morphology, viability and expression of specific genes brought about by the drug treatment.

Histological or immunological analyses that can be used with the array include, without limitation, a nucleic acid hybridization, PCR (such as in situ PCR), PRINS, ligase chain reaction, pad lock probe detection, histochemical in situ enzymatic detection, and the use of molecular beacons.

The tissue array technology can be used to directly collect specimens (tissues or cells) from humans, animals, cell lines, or other experimental systems. For example, when biopsy specimens are treated in a conventional manner in pathology laboratories, after fixation, the specimens are routinely inserted horizontally in a paraffin block. Therefore, it is very difficult, if not impossible to acquire specimens from such tissues into a tissue array. However, if multiple biopsy specimens obtained from surgery are directly fixed (and, if required, embedded in a suitable medium, such as paraffin) and then inserted directly vertically into a matrix, this would enable construction of a tissue array of biopsy specimens. Such an array would be useful for research purposes or in a clinical setting to e.g. monitor progression of premalignant lesions or monitor treatment responses (with molecular markers) from metastatic tumors that cannot be surgically removed.

Cytological specimens (such as fine needle aspirations, cervical cytology, blood specimens, isolated blood cells, urine cells etc.) can be either pelleted by centrifugation and then fixed and embedded for arraying as explained previously. Alternatively, cells can be fixed in a suspension, and directly inserted (e.g. pipetted) into holes in a matrix or embedded first, and then arrayed. This will provide an array of cells for research or for diagnostic purposes. This would enable rapid cytological diagnostics where multiple specimens from different patients can be screened simultaneously from a single slide, not only for their morphology, but for their molecular characteristics. This would also enable automation of the analysis, since a number of specimens can be screened with a microscope, automated image analysis system, scanner or associated expert systems at once. The use of such cellular preparations is particularly important for the diagnosis of hematological disorders, such as leukemias and lymphomas. This would also allow automation of lymphocyte typing from many patients at once, whose specimens are inserted in an array format for

immunophenotyping or for analysis by in situ hybridization. Screening of donated blood specimens for viral antigens, viral DNA or other pathogens in a blood bank could similarly be performed in an array format.

5 Arrays of tumor progression can also be constructed by collecting specimens from a subject at different stages of progression of the subject's tumor (such as progression to hormone refractory prostate cancer). Alternatively, tumors of different stages from different subjects can be collected and incorporated into the array. The array can also be used to follow the progression of pre-neoplastic lesions (such as the evolution of cervical neoplasia), and the effects of chemoprevention agents (such as the effects of antiestrogens on breast epithelium and breast cancer  
10 development).

In another embodiment, specimens from a transgenic or model organism can be obtained at different stages of development of the organism, such as different embryonic stages, or different ages after birth. This enables the study of things such as normal and abnormal embryonic development.

15 The biological analyses that are performed on the microarray sections can be any analysis performed on regular tissue sections. Arrays can also be assembled from one or more tumors at different stages of progression, such as normal tissue, hyperplasia, in situ cancer, invasive cancer, recurrent tumor, local lymph node metastases, or distant metastases.

An "EST" or "Expressed Sequence Tag" refers to a partial DNA or cDNA sequence, typically of between 50 and 500 sequential nucleotides, obtained from a genomic or cDNA library, prepared from a selected cell, cell type, tissue or tissue type, organ or organism, which  
20 corresponds to an mRNA of a gene found in that library. An EST is generally a DNA molecule.

"Specific hybridization" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g. total cellular) DNA or RNA. Stringent conditions are conditions under  
25 which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point  $T_m$  for the specific sequence at a defined ionic strength and pH.  
30

In view of the many possible embodiments to which the principles of the invention may be applied, it should be recognized that the illustrated embodiments are examples of the invention, and should not be taken as a limitation on the scope of the invention. Rather, the scope of the invention is defined by the following claims. We therefore claim as our invention all that  
35 comes within the scope and spirit of these claims.

We claim:

1. A method of parallel analysis of tissue specimens, comprising:  
obtaining a plurality of donor specimens;  
placing each donor specimen in an assigned location in a recipient array;  
5 obtaining a plurality of sections from the recipient array in a manner that each section contains a plurality of donor specimens that maintain their assigned locations;  
performing a different biological analysis of each section; and  
comparing the results of the different biological analyses in corresponding assigned locations of different sections to determine if there are correlations between the results of the  
10 different biological analyses at each assigned location.
2. The method of claim 1, wherein the donor specimen is obtained by boring an elongated sample from the donor specimen, which is placed in the assigned location in the recipient array.
3. The method of claim 1, wherein the donor specimen is from a tumor.
- 15 4. The method of claim 1, wherein the donor specimen is from a population of cells.
5. The method of claim 3, wherein the donor specimen is from a hematologic or cytological preparation.
6. The method of claim 1, wherein placing the donor specimen in an assigned location in the recipient array comprises forming an elongated receptacle in a donor block, and placing the  
20 elongated sample in the elongated receptacle of the recipient block.
7. The method of claim 6, wherein the elongated sample is placed in a receptacle having a cross-sectional size and shape complementary to a cross-sectional size and shape of the elongated sample.
8. The method of claim 7, wherein forming the elongated receptacle comprises forming a  
25 cylindrical bore in the recipient block, and the sample is obtained by boring a cylindrical tissue specimen from the donor block, wherein a diameter of the elongated receptacle is substantially the same as a diameter of the sample.
9. The method of claim 1, further comprising associating a clinical parameter with each assigned location in the recipient array.
- 30 10. The method of claim 1 wherein performing the different biological analysis on each section comprises performing different tests selected from the group of an immunological analysis and a nucleic acid hybridization.
11. The method of claim 10, further comprising determining whether there are correlations between clinical parameters, immunologic analysis and nucleic acid hybridization.
- 35 12. The method of claim 1, wherein the biological sample is a tissue specimen or cellular preparation.
13. A method of parallel analysis of identical arrays of tissue specimens, comprising:

forming a donor block comprising a biological specimen embedded in embedding medium;  
obtaining a plurality of elongated donor sample cores from the biological specimen;  
boring receptacle cores from a recipient embedding medium to form an array of elongated  
receptacles;

5       placing the donor sample cores in the elongated receptacles at assigned locations in the  
array;

sectioning the recipient embedding medium to obtain a cross-section of the donor sample  
cores in the array, while maintaining the assigned locations in the array in consecutive cross-  
sections;

10       performing a different biological analysis of each cross-section; and

comparing a result of each biological analysis in corresponding assigned locations of  
different sections to determine if there are correlations between the results of the different  
biological analyses at each assigned location.

14. The method of claim 13, further comprising comparing the results of the different  
15       biological analyses at each assigned location to clinical information about the biological specimen at  
the assigned location.

15. The method of claim 14, wherein the biological specimen is a tissue specimen from a  
tumor.

16. The method of claim 15, wherein the biological analyses are selected from the group  
20       consisting of a histologic analysis, an immunologic analysis, and a nucleic acid hybridization  
analysis.

17. The method of claim 13, further comprising aligning a thin tissue section above the  
donor block to identify an area of interest from which the donor sample core is taken.

18. The method of claim 13, wherein the elongated donor sample core is a substantially  
25       cylindrical core that has a diameter that is less than about 1 mm.

19. A cross-section of the donor sample cores obtained by the method of claim 13.

20. An apparatus for preparing specimens for parallel analysis of sections of biological  
material arrays, comprising:

a holder that can be positioned to maintain a tissue donor block in a donor position; and  
30       a reciprocal punch positioned in relation to the holder to punch a tissue specimen from the  
donor block in the donor position, wherein the holder is also capable of holding a recipient block in  
a recipient position, and the recipient block comprises an array of receptacles, each of which can be  
positioned in a preselected position in relation to the reciprocal punch to deliver a tissue specimen  
from the reciprocal punch into a receptacle in the preselected position.

21. The apparatus of claim 20, wherein the holder comprises an x-y positioning device  
35       that can be incrementally positioned to align sequential receptacles with the reciprocal punch.

22. The apparatus of claim 20, further comprising a stylet positioned for introduction into the reciprocal punch to expel the tissue specimen from the punch into one of the receptacles aligned with the punch.

23. The apparatus of claim 20, further comprising a positioner that positions a thin section  
5 slide over the donor block, to align structures of interest in the thin section slide with corresponding tissue specimen regions in the donor block.

24. The apparatus of claim 20, further comprising a separate reciprocal punch capable of being positioned in a fixed position relative to the recipient block for forming the array of receptacles in the recipient block.

10 25. The apparatus of claim 24, further comprising a recorder for recording the positions of the receptacles in the recipient block.

26. The apparatus of claim 25, wherein the recorder is a computer implemented system for recording the positions of the receptacles, and an identification of the tissue specimen that is placed in each receptacle.

15 27. A computer implemented system for parallel construction of consecutive sections of tissue arrays, comprising:

an x-y positioning platform for moving a tray or a receptacle punch relative to a plurality of coordinates that correspond to positions in a recipient block array;

20 the receptacle punch positioned in punching relationship with respect to the positioning platform, such that the receptacle punch can punch a receptacle core from a recipient block on the positioning platform,

a donor punch positioned in a punching relationship with respect to the positioning platform, such that the donor punch can punch a donor specimen from a donor block on the positioning platform, wherein the receptacle core has a diameter that is substantially the same as the  
25 diameter of the donor specimen;

a stylet that is selectively alternatively aligned with the donor punch and the recipient punch, for displacing contents of the receptacle punch after a receptacle core is punched from the recipient block, and for displacing contents of the donor punch into receptacles of the recipient block array after a donor specimen is punched from the donor block; and

30 wherein the system records an identification of tissue in the receptacles of the recipient array.

28. The computer implemented system of claim 27, further comprising a microscope for viewing the donor block, and locating a structure of interest in a reference slide aligned with the donor block.

35 29. The computer implemented system of claim 27, wherein the system punches a receptacle core from the recipient block and displaces the receptacle core from the receptacle punch with the stylet, then punches a donor specimen from the donor block, aligns the donor punch with a

selected receptacle in the recipient block, and displaces the donor specimen into the selected receptacle.

30. A method of analyzing ex vivo tissue specimens, comprising punching an elongated tissue sample from the ex vivo tissue specimen, and subjecting the sample to a biological analysis.

5 31. The method of claim 30, wherein punching the elongated tissue sample from the tissue specimen comprises placing the tissue specimen in a holder below a reciprocal punch, and advancing the reciprocal punch into a predetermined location of the tissue specimen.

32. The method of claim 31, further comprising fixing the tissue specimen and placing the tissue specimen in an embedding medium prior to punching.

10 33. The method of claim 31, wherein the predetermined location of the tissue specimen is determined by examining a thin section cut from the embedding medium.

34. The method of claim 1, further comprising using a nucleic acid microarray to identify a biomarker to be used in a biological analysis on the recipient array.

15 35. The method of claim 34, wherein the nucleic acid array is a cDNA or oligonucleotide microarray.

36. The method of claim 35, wherein the biomarker is selected by a high throughput immunological or genetic analysis.

37. The method of claim 34, wherein the biomarker comprises a marker for gene expression.

20 38. The method of claim 34, wherein the biomarker comprises a structural or numerical alteration of a chromosome, chromosomal region, gene, gene fragment or locus, or a gene function alteration.

39. The method of claim 1, wherein comparing the results comprises determining if there is an alteration of a gene by examining a marker for protein expression or other gene alteration.

25 40. The method of claim 39, wherein the alteration of protein expression is determined by an immunologic analysis.

41. The method of claim 39, wherein the alteration is an overexpression of vimentin in renal cell carcinoma, or an overexpression of IGFBP2 in human prostate cancer, or an overexpression of PDGFB in breast, lung, colon, testicular, endometrial or bladder cancer.

30 42. A method of analyzing genetic changes or gene expression in a tissue specimen, comprising:

screening multiple genes in a tissue specimen, with a nucleic acid array that detects which genes are abnormally expressed in the tissue specimen; and

35 screening multiple tissue specimens in a tissue array, with a nucleic acid probe to detect which genes are abnormally expressed in the tissue specimens;

wherein the result of screening multiple genes is used to select the nucleic acid probe to screen the multiple tissue specimens, or wherein the result of screening multiple tissue specimens is used to select the array that detects which genes are abnormally expressed.

43. The method of claim 42, wherein screening multiple genes comprises performing a high throughput genomic technique.

44. The method of claim 42, wherein the high throughput genomic technique is selected from the group of cDNA hybridization, genomic DNA sequencing, protein sequencing, RDA, differential display, subtractive hybridization, SAGE, hybridization based sequencing, and cDNA and oligonucleotide arrays.

45. The method of claim 42, wherein screening multiple genes to determine which genes are abnormally expressed comprises searching databases and other biomedical sources of information.

46. The method of claim 42, wherein screening the multiple genes comprises using a cDNA array to determine which genes are abnormally expressed.

47. The method of claim 42, wherein screening the multiple genes comprises providing a DNA array which is assayed for a gene amplification, deletion, mutation, polymorphism, methylation change or other alteration of gene structure or function, or a genetic or molecular marker that reflects this change.

48. The method of claim 47, wherein the DNA array is a microarray that contains target loci that undergo differential expression in cancer.

49. The method of claim 42, wherein screening multiple genes obtained from a single tissue specimen comprises hybridizing nucleic acid molecules associated with a cell with the DNA array that contains target loci that undergo differential expression, and determining which target loci indicate differential expression of a gene in the cell.

50. The method of claim 49, further comprising selecting a target locus that undergoes differential expression, providing a probe that includes or is complementary to at least a portion of the target locus, and using the probe to screen the multiple tissue specimens.

51. The method of claim 1, wherein the results of the different biological analyses are used to:

- a. evaluate a reagent for disease diagnosis or treatment;
- b. identify a prognostic marker for cancer;
- c. prioritize targets for drug development;
- d. assess or select therapy for a disease type; or
- e. find a biochemical target for medical therapy.

52. The method of claim 51, wherein evaluating a reagent for disease diagnosis or treatment comprises evaluating a reagent selected from the group of antibodies, genetic probes, and antisense molecules.

53. The method of claim 52, wherein evaluating a reagent for disease diagnosis or treatment comprises evaluating a reagent selected from the group of biological inhibitors, biological enhancers, or other biological modulators.

54. The method of claim 51, wherein identifying a prognostic marker for cancer  
5 comprises selecting a marker associated with a poor clinical outcome.

55. The method of claim 51, wherein selecting therapy for the subject comprises selecting an antineoplastic therapy that is associated with a particular biological analysis outcome.

56. The method of claim 55, wherein the particular biological analysis outcome is an oncogene amplification, deletion, translocation, mutation or other genetic rearrangement which is  
10 correlated with a clinical response to a particular therapy.

57. The method of claim 1, wherein the donor specimens are specimens from one or more tumors.

58. The method of claim 57, wherein the donor specimens are specimens from one or more tumors selected from the group of breast, prostate and bladder cancer.

59. The method of claim 57, wherein the donor specimens are specimens from a plurality  
15 of tumors all of the same organ or histologic type.

60. The method of claim 56, wherein the donor specimens are specimens from a plurality of tumors from different organs or tissue types.

61. A method of constructing a specimen array, comprising:  
20 providing cellular specimens in a matrix, with the specimens positioned at predetermined known positions, such that when multiple copies of the matrix are provided, a two dimensional array of specimens is presented on each copy, with each specimen at a predetermined position in the matrix, and wherein each matrix has a third dimension so that when sequential copies of the matrix are provided, the specimens maintain a predetermined relationship in the array; and  
25 exposing sequential copies of the matrix to an agent which interacts with the specimens of the array, to identify those specimens which share a common biological property.

62. The method of claim 62, wherein the specimens are provided in an elongated form, and multiple copies of the matrix are made by cutting sections from a three dimensional array into predetermined sections, such that as sequential sections of the matrix are cut, the specimens  
30 maintain the predetermined relationship.

63. The method of claim 61, wherein the common biological property is a morphologic or molecular characteristic.

64. The method of claim 61, wherein the biological characteristic is a presence or absence, or altered level of expression, of a gene or protein, alteration of copy number, structure or  
35 function of a gene, genetic locus, chromosomal region or chromosome.

65. The method of claim 62, wherein the biological characteristic is a specific reaction with an antibody specific for a specimen of interest.



66. The method of claim 61, wherein the common biological property is correlated with an other characteristic of the specimens.

67. The method of claim 66, wherein the other characteristic of the specimens includes clinical information about a subject from whom each specimen was taken.

5        68. The method of claim 67, wherein the clinical information includes one or more of clinical course, treatment response, histological type or grade, tumor stage, age and sex of the subject from whom each specimen was taken.

69. The method of claim 62, wherein the cellular specimen is a tissue specimen.

70. The method of claim 61, wherein the cellular specimen is a cellular suspension.

10       71. The method of claim 70, wherein the specimen is a liquid cellular specimen that has been converted into a solid cellular specimen.

72. The tissue array of claim 61.

73. The tissue array of claim 62.

15       74. The method of claim 61, further comprising exposing a gene array to a candidate specimen, and selecting a candidate probe for the specimen array.

75. The method of claim 61, wherein the common biological property is her-2 status, and the method further comprises selecting a therapy based on her-2 status.

76. The method of claim 61, wherein the specimens comprise a tissue from a model or transgenic organism.

20       77. The method of claim 76, wherein the specimens comprise tissue from the model or transgenic organism at different stages of development.

78. The method of claim 61, wherein the specimens comprise animal, yeast or bacterial cells.

25       79. The method of claim 78, wherein the cells are in a liquid suspension which is applied to a surface of a support.

80. The method of claim 79, wherein the liquid suspension is from a body fluid.

81. The method of claim 80, wherein the body fluid is selected from the group of a needle aspiration, a cytology specimen, urine, and ascitic fluid.

82. The method of claim 77, wherein the cells comprise a sample of a liquid malignancy.

30       83. The method of claim 78, wherein the liquid malignancy comprises a hematological malignancy.

84. The method of claim 78, wherein the cells are from one or more cell lines.

85. The method of claim 61, wherein the specimens comprise specimens from one or more tumors at different stages of progression.

35       86. The method of claim 81, wherein the one or more tumors are prostate cancer tumors.

87. A method of screening for cancer in a specimen, comprising determining whether platelet derived growth factor beta (PDGFB), FGFR2, MYBL2, or IGFBP2 is expressed, overexpressed or amplified in the specimen.

88. A method of screening for cancer in a specimen, comprising determining:
- 5       whether PDGFB is overexpressed or amplified in the specimen, wherein the cancer is selected from the group of lung, bladder and endometrial cancer;
- whether FGFR2 is amplified in the specimen, wherein the cancer is breast cancer;
- whether IGFBP2 is expressed in the specimen, wherein the cancer is hormone refractory prostate cancer;
- 10       whether MYBL2 is amplified and expressed in breast cancer; and
- whether MYC, AR and cyclin-P1 are amplified in prostate cancer.

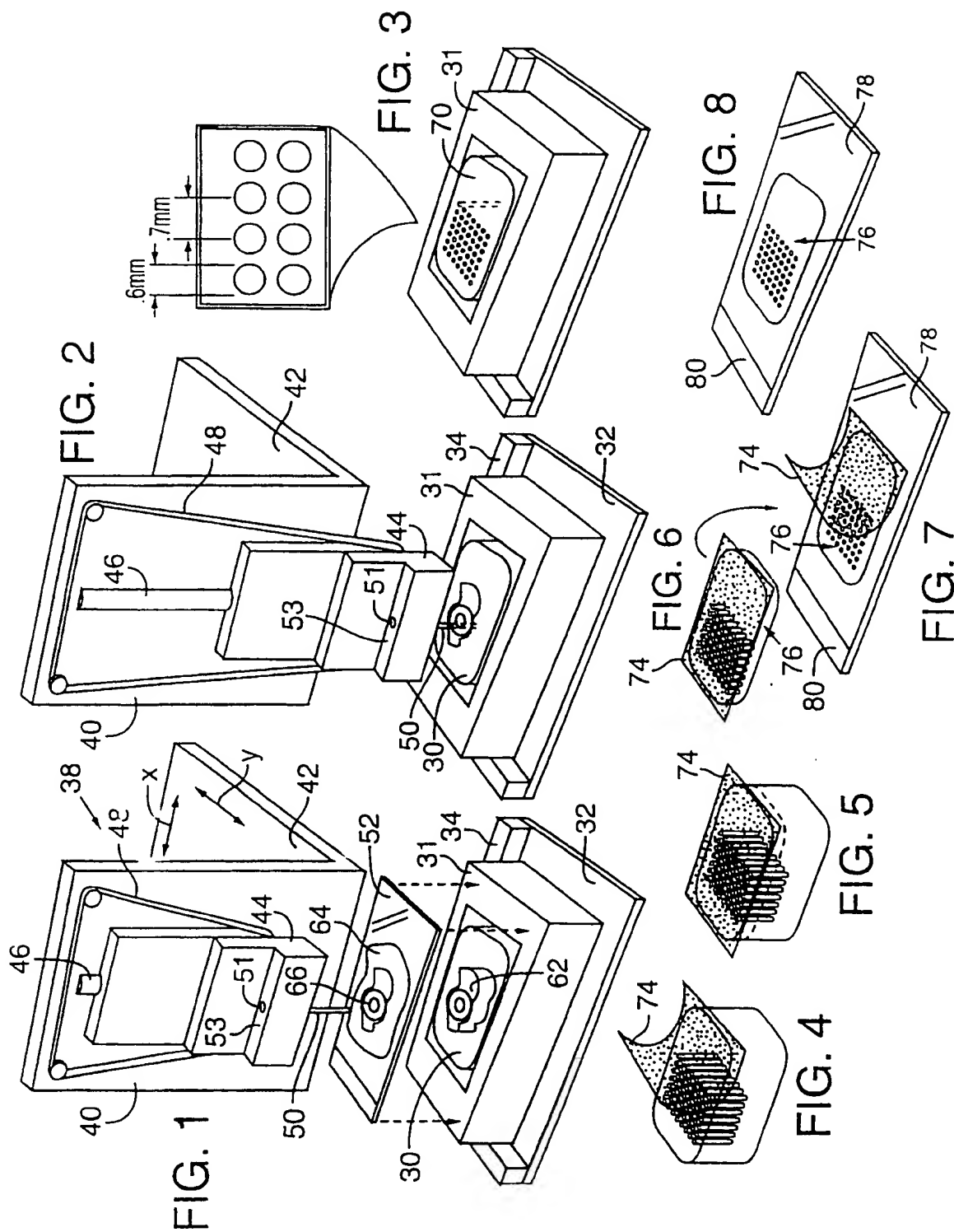
89. The method of claim 88, wherein the method comprises determining whether PDGFB is overexpressed or amplified in the specimen, wherein the cancer is selected from the group of lung, bladder and endometrial cancer.

- 15       90. The method of claim 88, wherein the method comprises determining whether FGFR2 is amplified in the specimen, wherein the cancer is breast cancer.

91. The method of claim 88, comprising determining whether IGFBP2 is expressed in the specimen, wherein the cancer is hormone refractory prostate cancer.

- 20       92. The method of claim 88, comprising determining whether MYBL2 is amplified and expressed in breast cancer.

93. The method of claim 88, comprising determining whether MYC, AR and cyclin-P1 are amplified in prostate cancer.



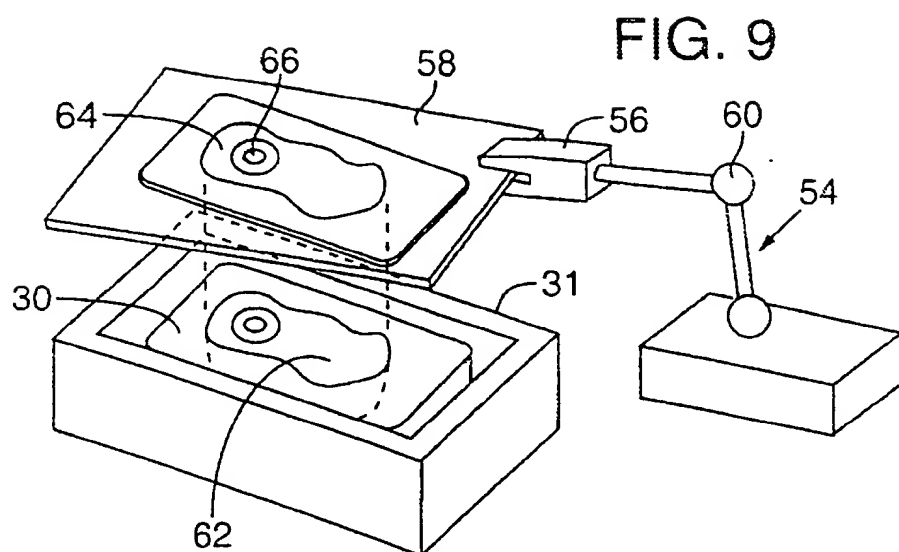


FIG. 10A



FIG. 10B

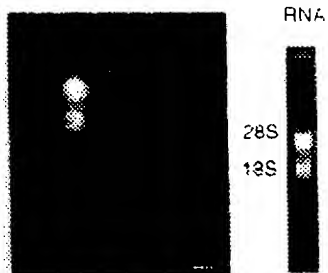


FIG. 10C

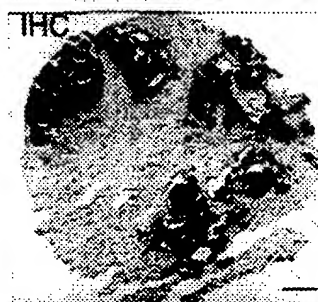


FIG. 10D

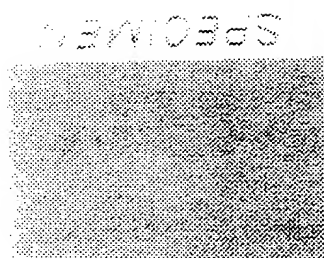


FIG. 10E

FIG. 11

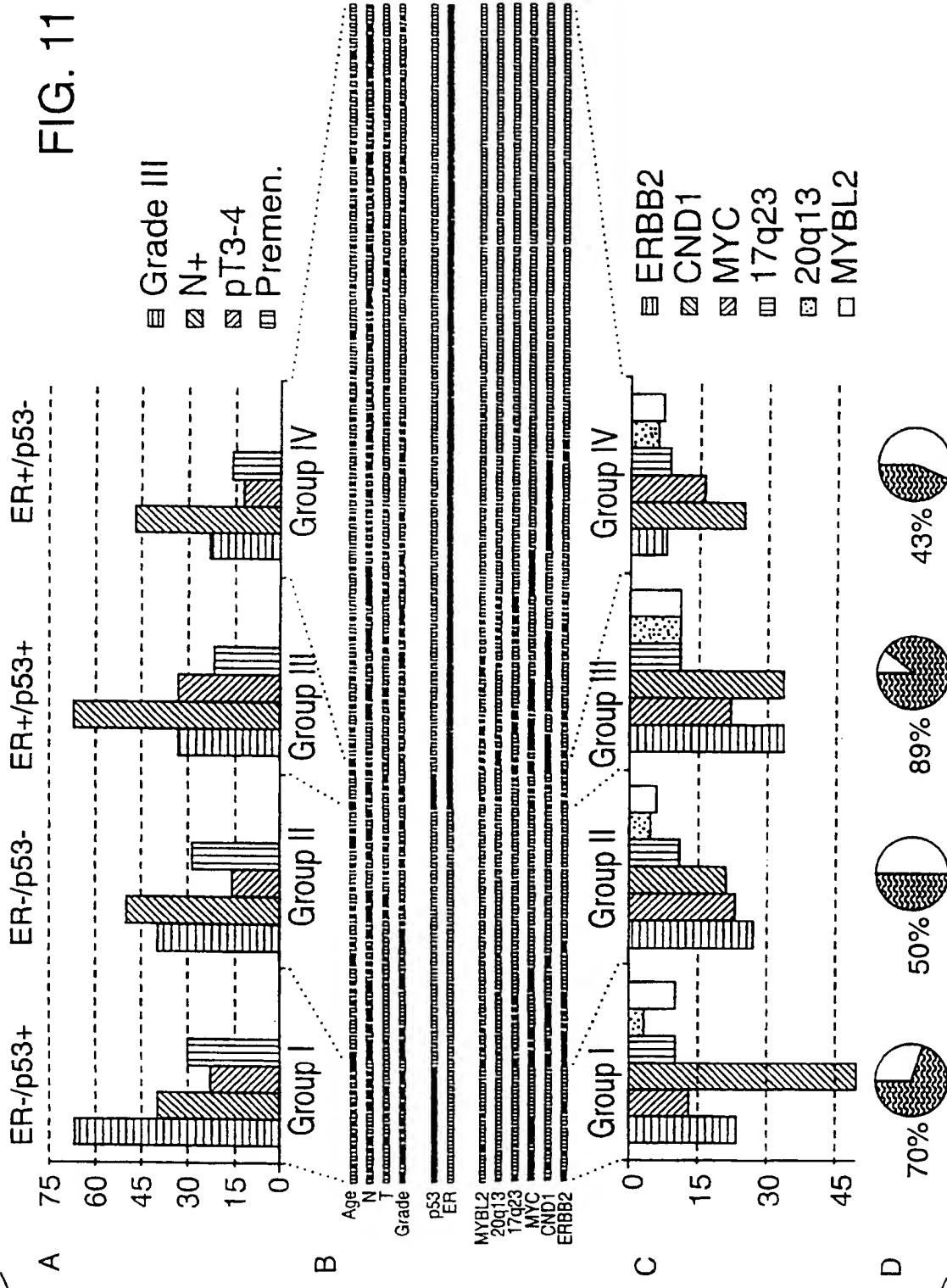


FIG. 12

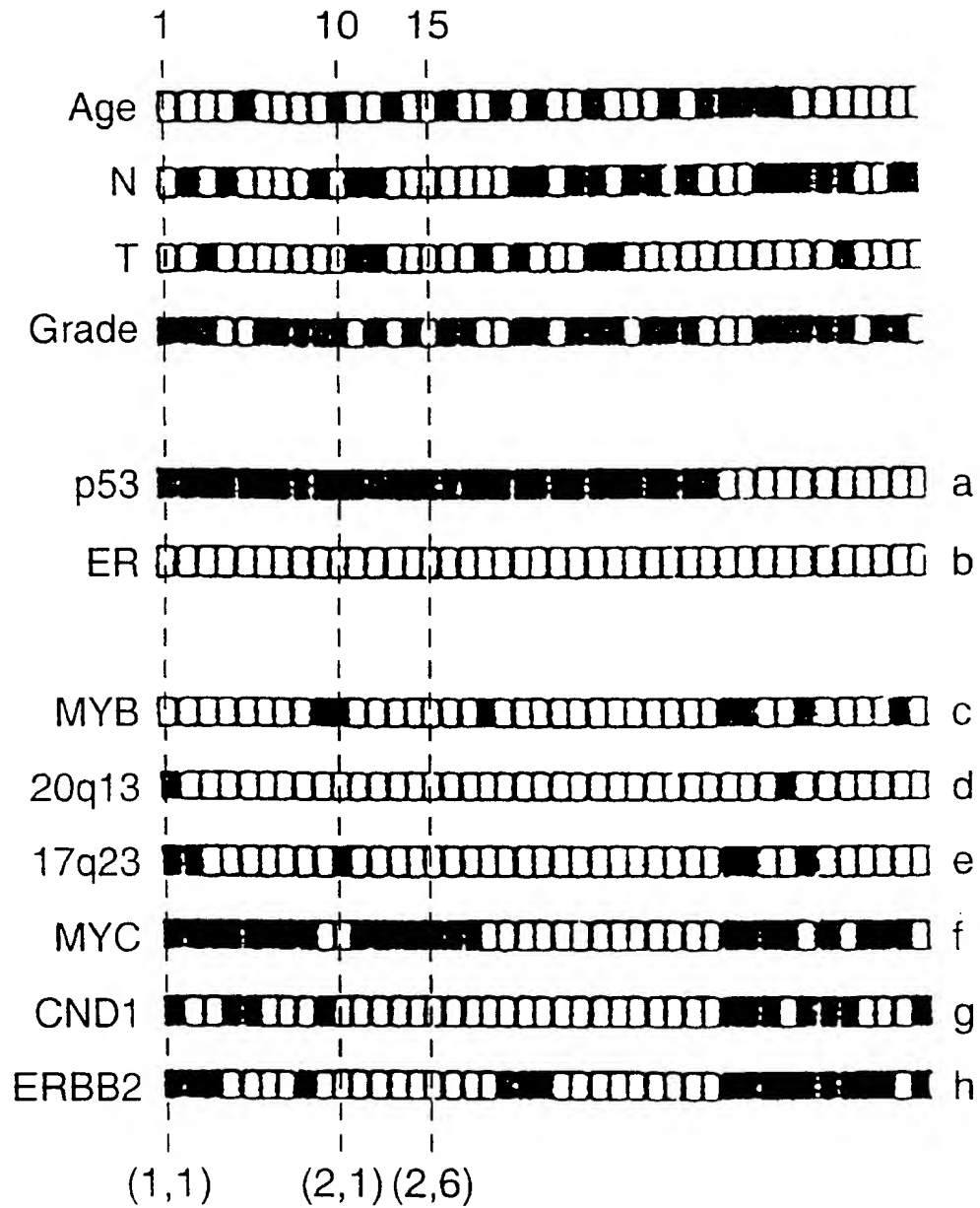


FIG. 13

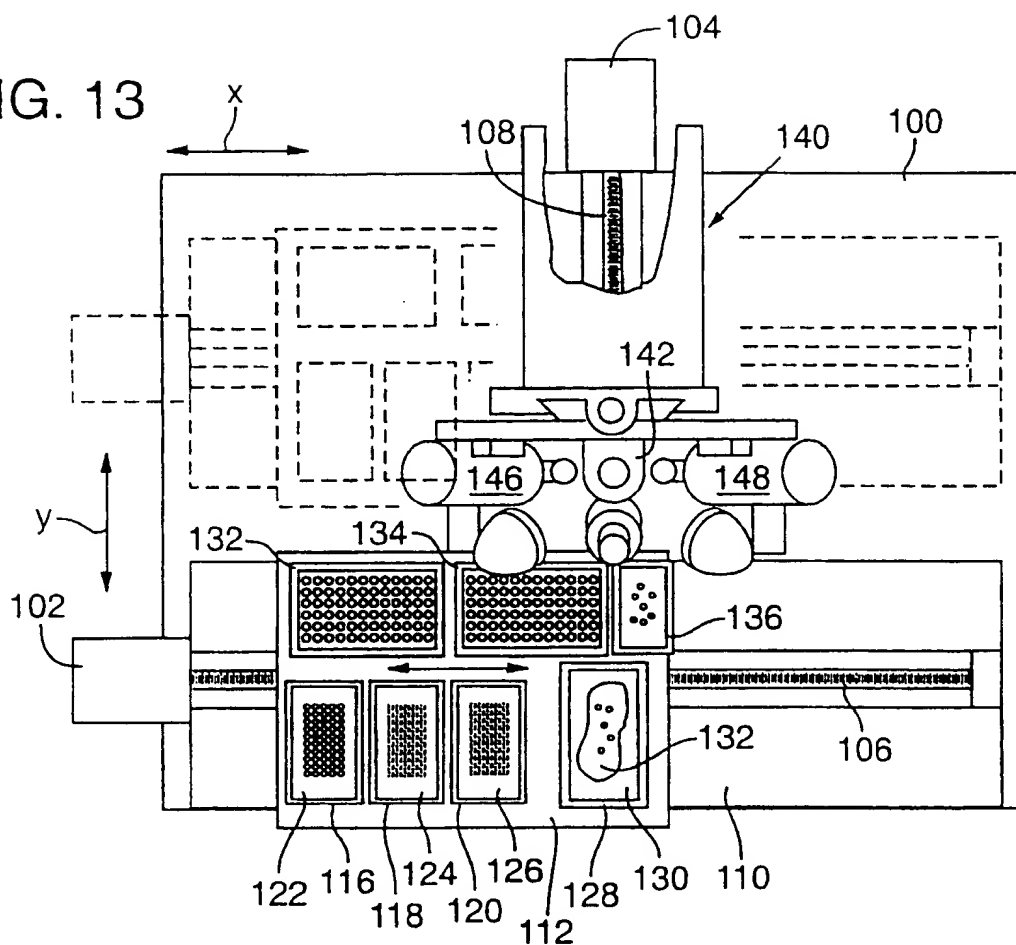
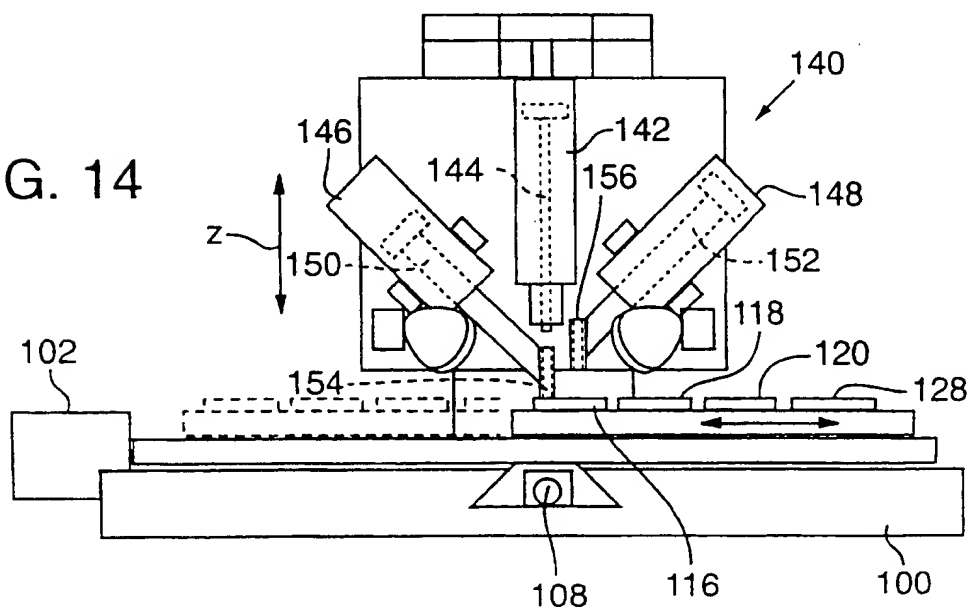
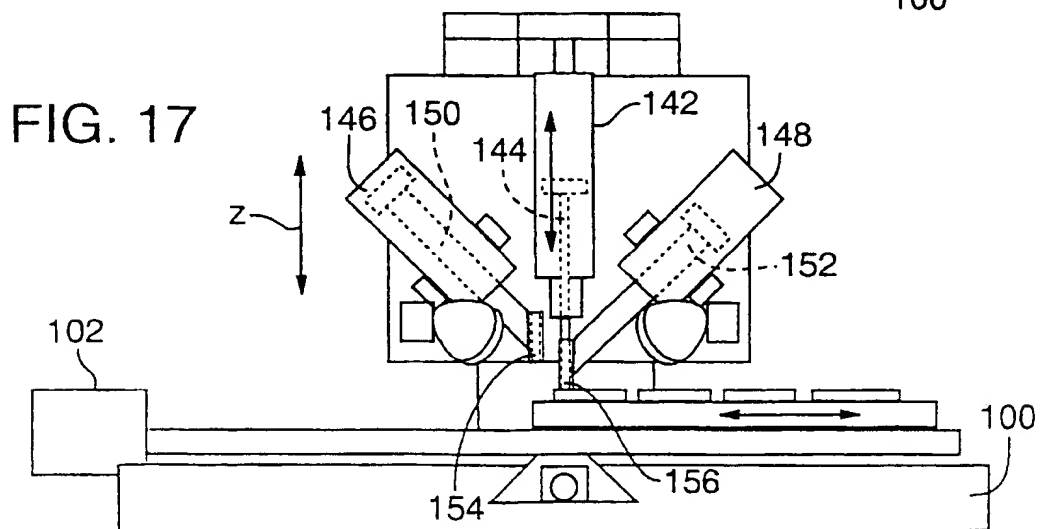
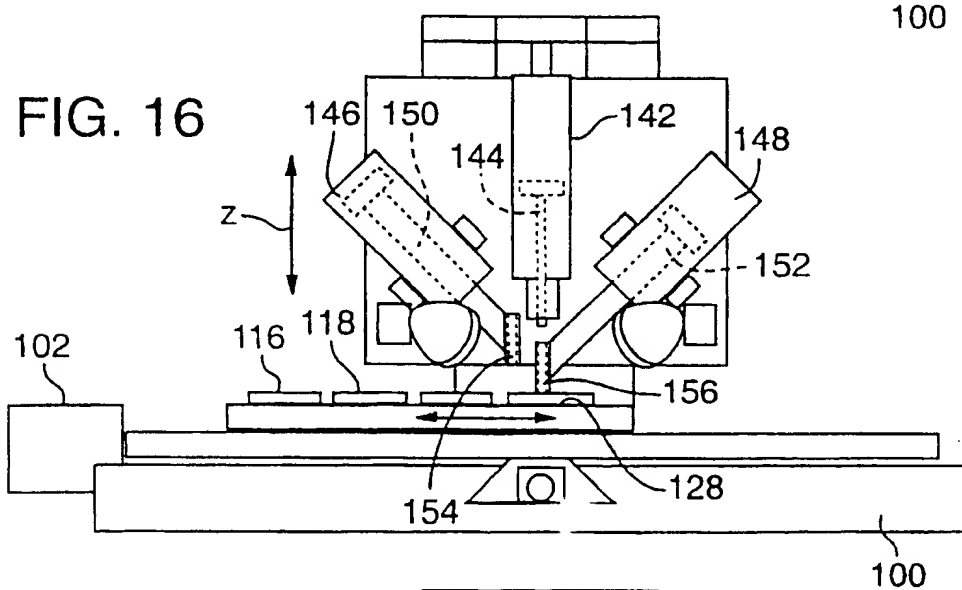
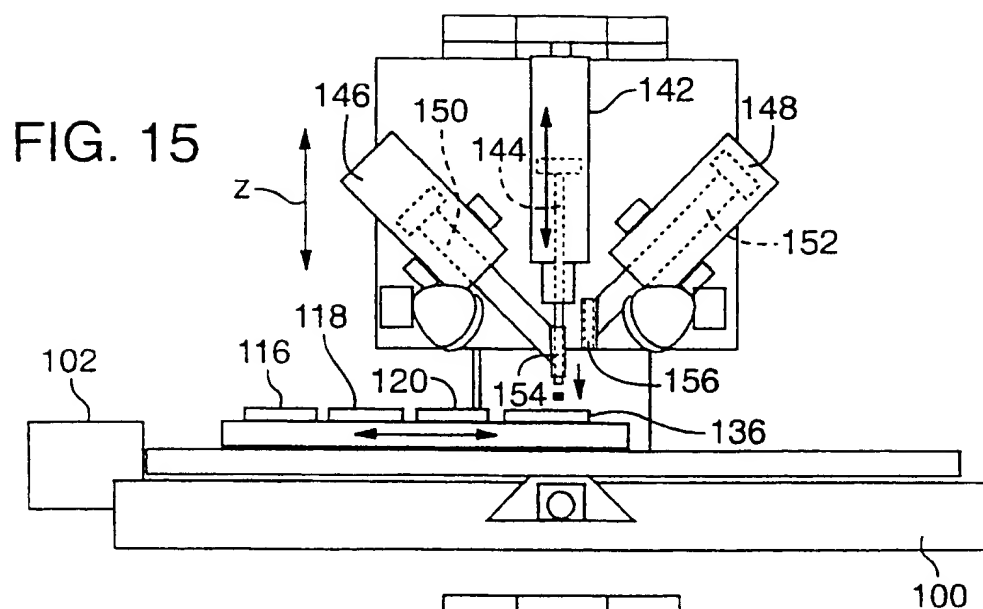
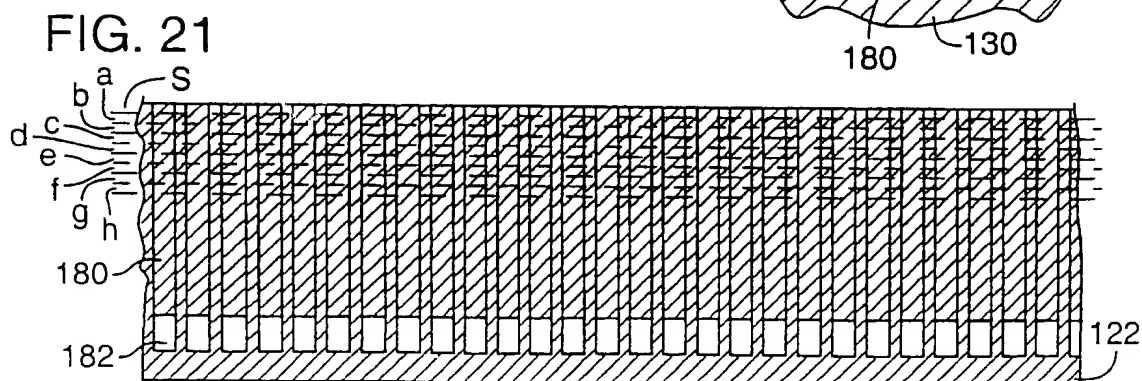
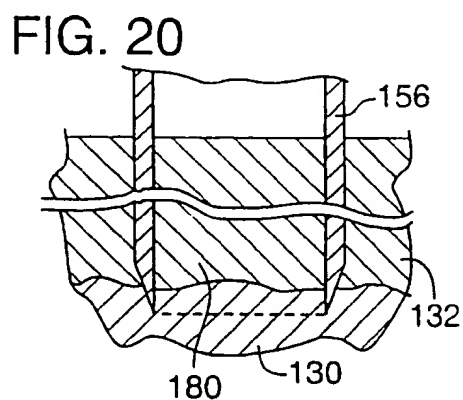
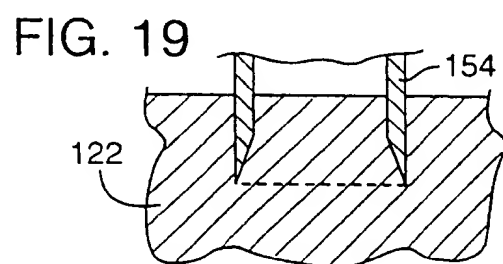
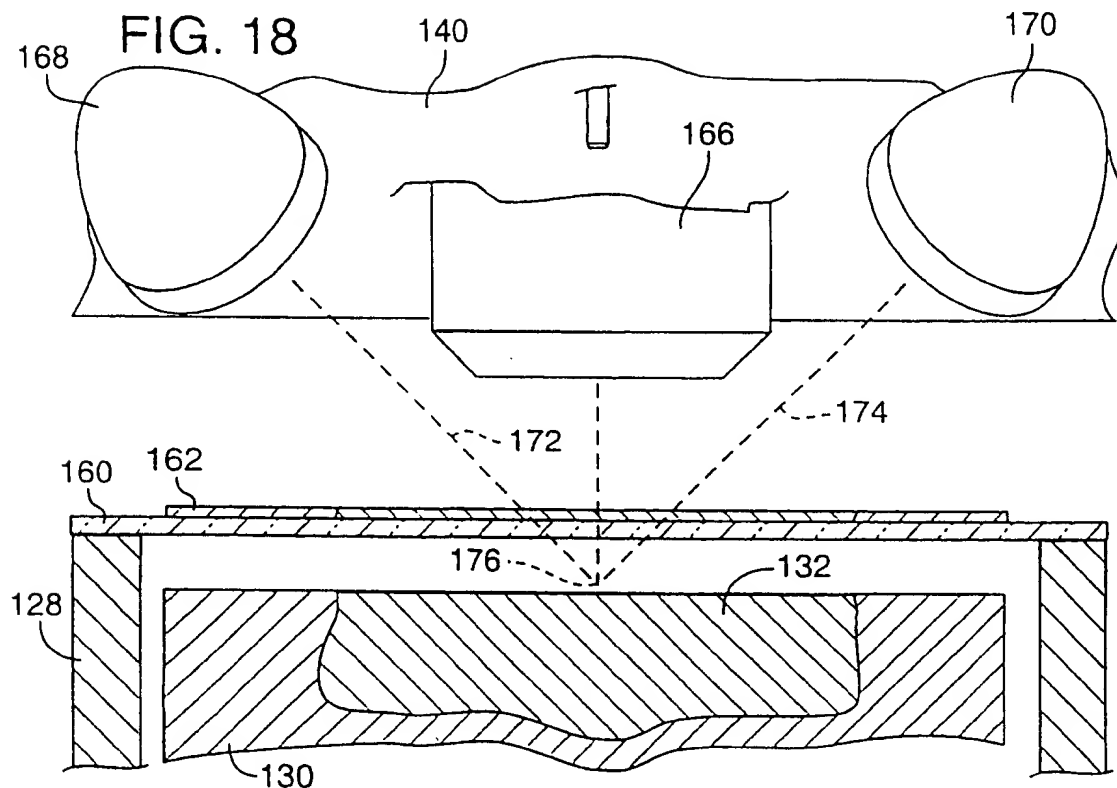


FIG. 14









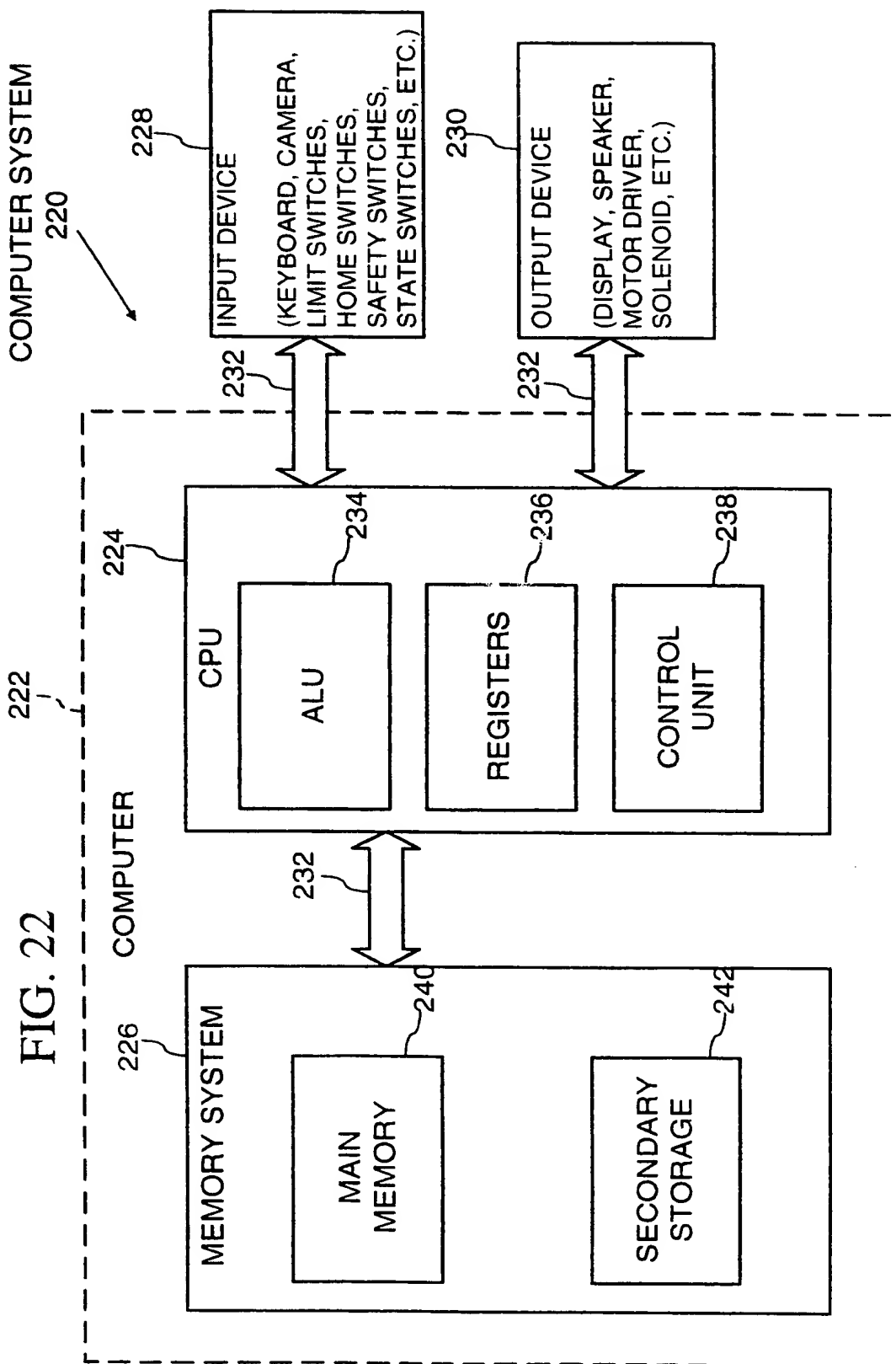


Fig. 23

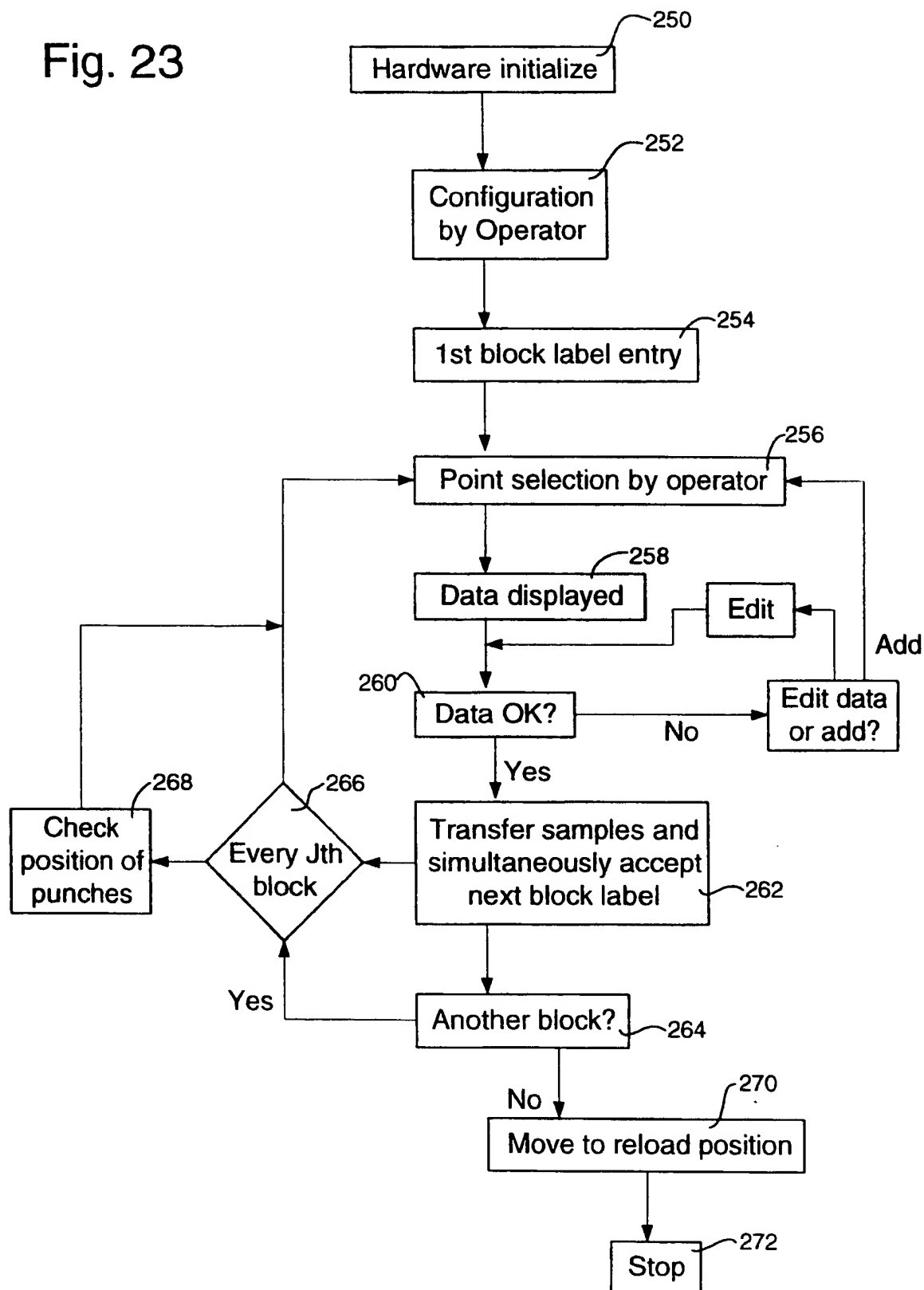


FIG. 24

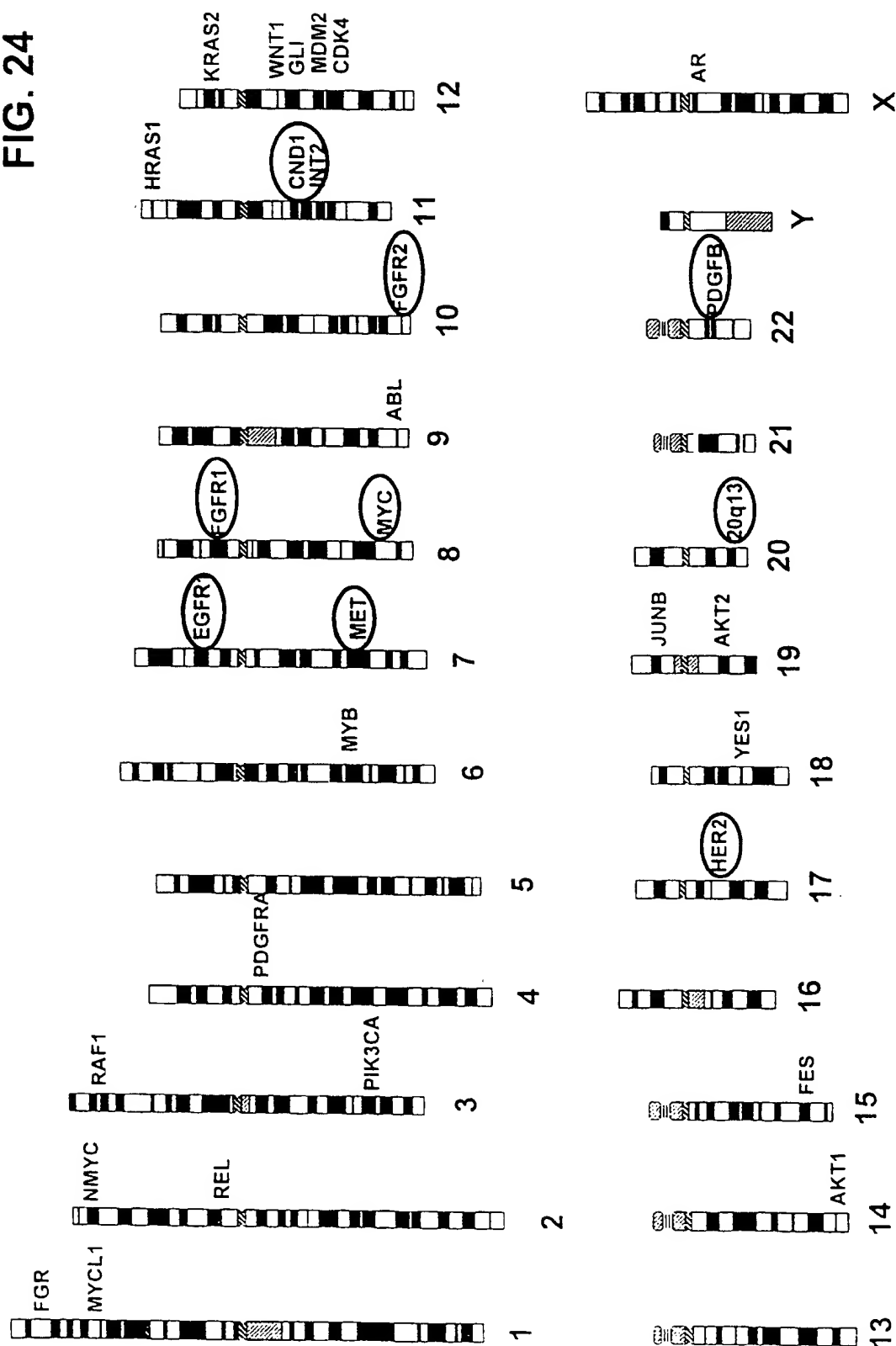
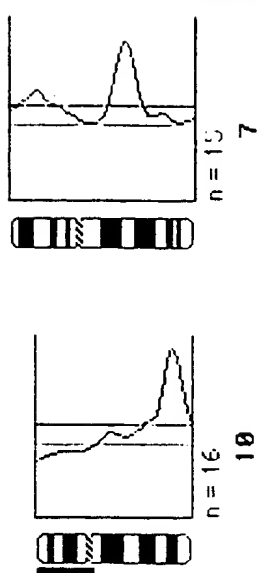
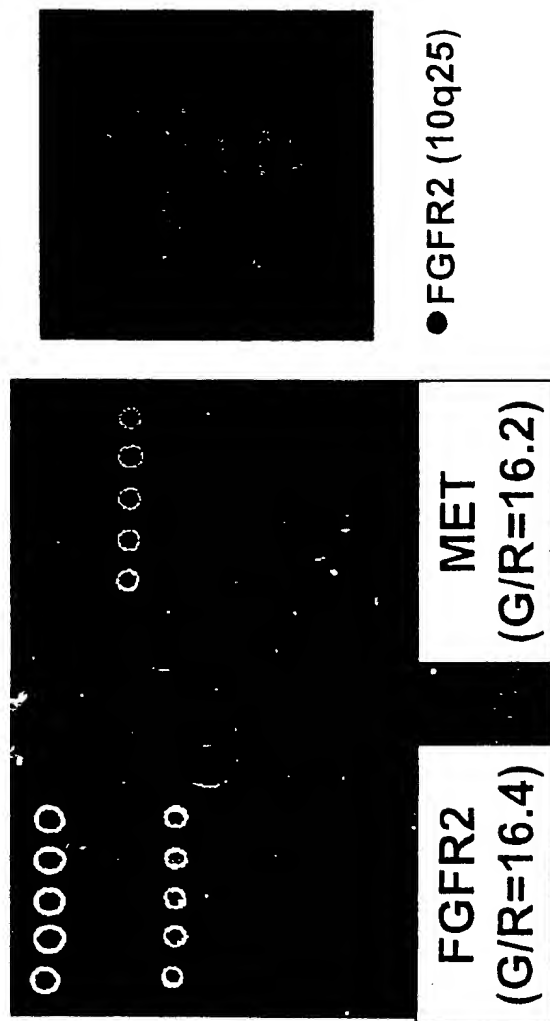


FIG. 25



FGFR2  
10q25-q26

MET  
7q21-q22



● FGFR2 (10q25)

The diagram illustrates the process of microarray data analysis. It features a grid of microarray spots, a magnified view of a single spot, and a pie chart showing that 4.5% of the spots are amplified.

**Breast cancer microarray n=153)**

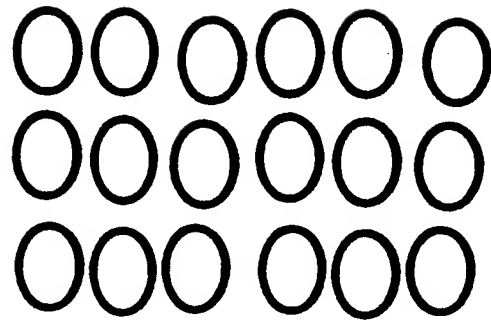
4.5% / amplified

FIG. 27

# *DNA chip*



1 tumor

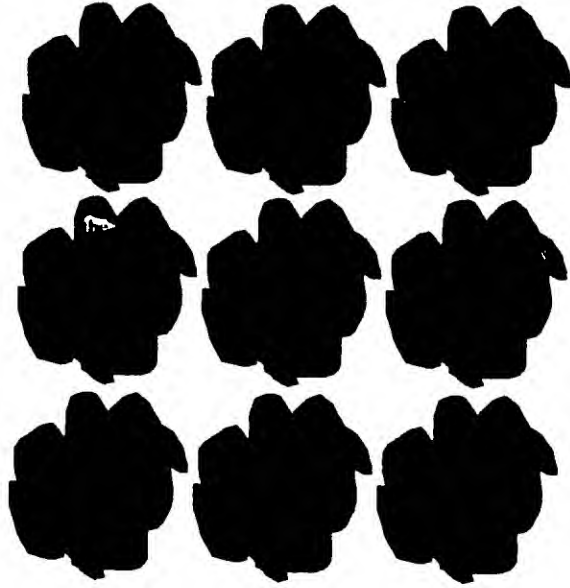


100's of clones

# *Tissue chip*

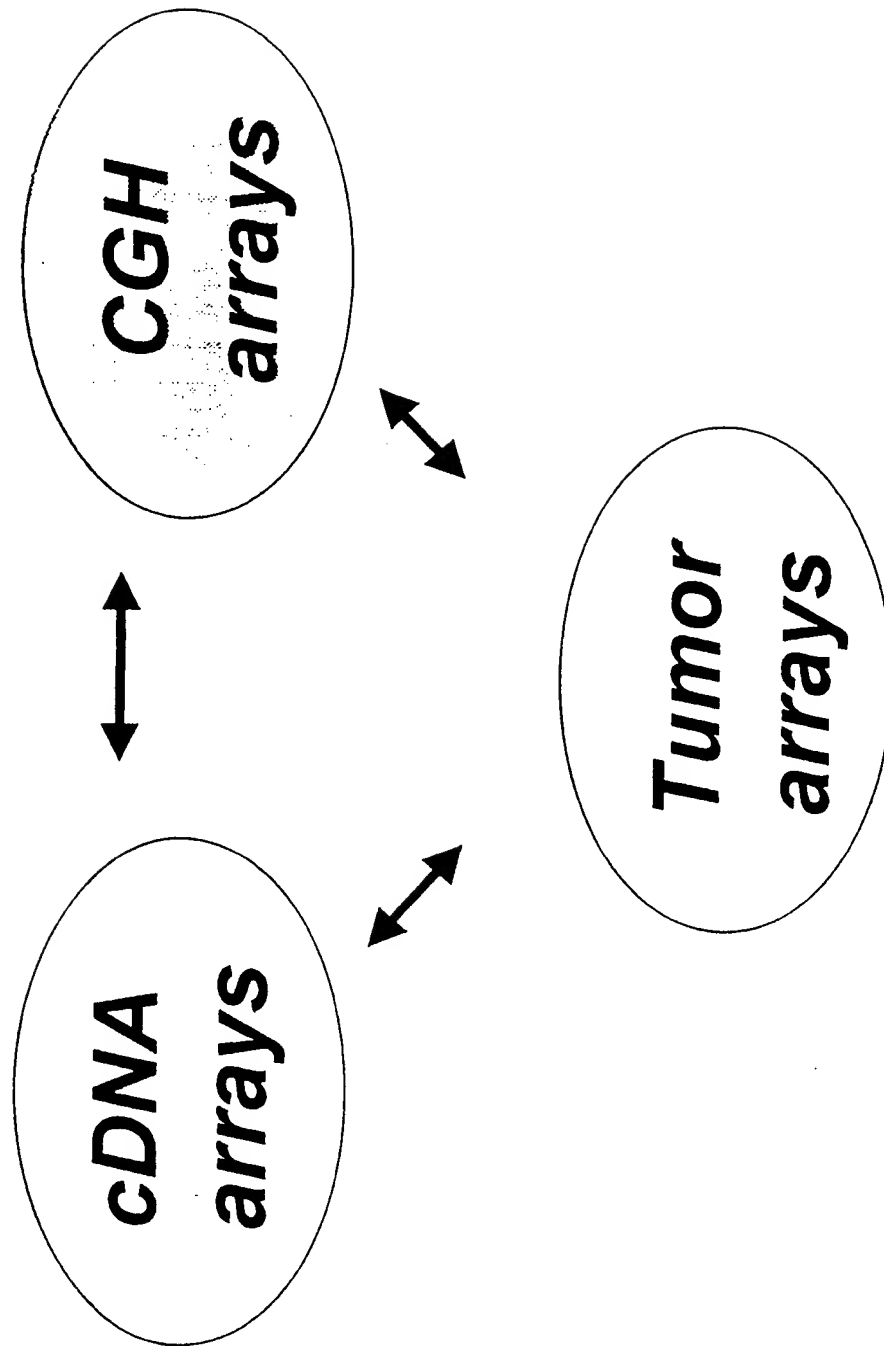


1 probe



100's of tumors

FIG. 28 **Biochip technologies**





# INTERNATIONAL SEARCH REPORT

In national Application No. PCT/US 99/04000

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> G 01 N 33/50, G 01 N 33/543, G 01 N 33/574, G 01 N 1/28, G 02 B 21/34, C 12 Q 1/04, C 12 Q 1/24, C 12 Q 1/28 According to International Patent Classification (IPC) or to both national classification and IPC: 6		
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) G 01 N, G 02 B, C 12 Q Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5002377 A (BATTIFORA et al.) 26 March 1991, abstract, claims. --	1-19, 61-73
A	US 4914022 A (FURMANSKI et al.) 03 April 1990, abstract, claims. --	2-19, 61-73
A	US 4820504 A (BATTIFORA) 11 April 1989, abstract, claims. --	61-73
A	US 5700637 A (SOUTHERN) 23 December 1997, abstract, claims. ----	1, 34-50, 87-93
<input type="checkbox"/> Further documents are listed in the continuation of box C. <input type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : 'A' document defining the general state of the art which is not considered to be of particular relevance 'E' earlier document but published on or after the international filing date 'L' document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) 'O' document referring to an oral disclosure, use, exhibition or other means 'P' document published prior to the international filing date but later than the priority date claimed 'T' later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention 'X' document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone 'Y' document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. '&' document member of the same patent family		
Date of the actual completion of the international search 18 June 1999		Date of mailing of the international search report 23. 07. 99
Name and mailing address of the ISA European Patent Office, P.O. Box 5318 Patentlaan 2 NL - 2220 HV Rijswijk Tel.: (+31-70) 340-2040, Tr. 31 651 epo nl, Fax: (+31-70) 340-3916		Authorized officer SCHNASS e.h.

Form PCT/ISA/210 (second sheet) (July 1992)

## ANHANG

zum internationalen Recherchen-  
bericht über die internationale  
Patentanmeldung Nr.

## ANNEX

to the International Search  
Report to the International Patent  
Application No.

## ANNEXE

au rapport de recherche inter-  
national relatif à la demande de brevet  
international n°

PCT/US 99/04000 SAE 227716

In diesem Anhang sind die Mitglieder  
der Patentfamilien der im obenge-  
nannten internationalen Recherchenbericht  
angeführten Patentedokumente angegeben.  
Diese Angaben dienen nur zur Unter-  
richtung und erfolgen ohne Gewähr.

This Annex lists the patent family  
members relating to the patent documents  
cited in the above-mentioned inter-  
national search report. The Office is  
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La présente annexe indique les  
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In Recherchenbericht angeführtes Patentedokument Patent document cited in search report Document de brevet cité dans le rapport de recherche	Datum der Veröffentlichung Publication date Date de publication	Mitglied(er) der Patentfamilie Patent family member(s) Membres(s) de la famille de brevets	Datum der Veröffentlichung Publication date Date de publication
US A 5002377	26-03-1991	AU A1 37890/89 AU B2 629838 AU A1 30453/92 AU A1 30454/92 AU B2 646984 AU B2 653280 CA A1 1322539 DE C0 68919136 DE T2 68919136 EP A2 350189 EP A1 350189 EP B1 350189 JP A2 2161334	11-01-1990 15-10-1992 11-03-1993 09-04-1993 10-03-1994 22-09-1994 28-09-1993 08-12-1994 24-05-1995 10-01-1990 29-05-1991 02-11-1994 21-06-1990
US A 4914022	03-04-1990	keine - none - rien	
US A 4820504	11-04-1989	AT E 91788 AU A1 68697/87 AU B2 606329 CA A1 1295218 DE C0 3786572 DE T2 3786572 DK A0 687/87 DK A 687/87 EP A2 238190 EP A2 238190 EP B1 238190 ES AF 2004874 FI A0 870578 FI A 870578 IL A0 81529 JP A2 63132163 NO A0 870535 NO A 870535 NZ A 219237 PT A 84269 ZA A 8700925	15-09-1993 15-08-1987 07-03-1991 04-03-1992 26-03-1993 02-12-1993 11-02-1987 13-08-1987 23-09-1987 23-08-1989 21-07-1993 16-02-1989 11-02-1987 13-08-1987 16-09-1987 04-06-1988 11-02-1987 13-08-1987 26-10-1990 01-03-1987 27-01-1988
US A 5700637	23-12-1997	AT E 110790 DE C0 68917879 DE T2 68917879 EP A1 373203 EP B1 373203 GB A0 8810400 JP T2 3505157 NO A1 8910977	15-09-1994 06-10-1994 05-01-1995 20-06-1990 31-08-1994 08-06-1988 14-11-1991 16-11-1989



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(54) Title: CELLULAR ARRAYS FOR RAPID MOLECULAR PROFILING			
(57) Abstract			
<p>A method is disclosed for rapid molecular profiling of tissue or other cellular specimens by placing a donor specimen in an assigned location in a recipient array, providing copies of the array, and performing a different biological analysis of each copy. In one embodiment, the copies of the array are formed by placing elongated specimens in a three dimensional matrix, and cutting sections from the matrix to form multiple copies of a two dimensional array that can then be subjected to the different biological analyses. Alternatively, the array can be formed from cell suspensions such that identical multiple copies of an array are formed, in which corresponding positions in the copies of the array have samples from the same or similar specimen. The results of the different biological analyses are compared to determine if there are correlations between the results of the different biological analyses at each assigned location. In some embodiments, the specimens may be tissue specimens from different tumors, which are subjected to multiple parallel molecular (including genetic and immunological) analyses. The results of the parallel analyses are then used to detect common molecular characteristics of the tumor type, which can subsequently be used in the diagnosis or treatment of the disease. The biological characteristics of the tissue can be correlated with clinical or other information, to detect characteristics associated with the tissue, such as susceptibility or resistance to particular types of drug treatment. Other examples of suitable tissues which can be placed in the matrix include tissue from transgenic or model organisms, or cellular suspensions (such as cytological preparations or specimens of liquid malignancies or cell lines).</p>			

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**AMENDED CLAIMS**

[received by the International Bureau on 13 September 1999 (13.09.99);  
original claims 1-93 replaced by new claims 1-85 (7 pages)]

1. A method of parallel analysis of biological specimens, comprising:  
obtaining a plurality of donor specimens;  
placing each donor specimen in an assigned location in a recipient array;  
obtaining a plurality of copies of the recipient array in a manner that each copy contains a plurality of donor specimens that maintain their assigned locations;  
performing a biological analysis of each copy; and  
comparing the results of the biological analysis in corresponding assigned locations of different copies to determine if there are correlations between the results of the biological analysis at each assigned location.
2. The method of claim 1, wherein the donor specimen is obtained by boring an elongated sample from the donor specimen, which is placed in the assigned location in the recipient array.
3. The method of claim 1, wherein the donor specimen is from a tumor.
4. The method of claim 1, wherein the donor specimen is from a population of cells.
5. The method of claim 3, wherein the donor specimen is from a hematological or cytological preparation.
6. The method of claim 1, wherein placing the donor specimen in an assigned location in the recipient array comprises forming an elongated receptacle in a donor block, obtaining an elongated donor specimen, and placing the elongated donor specimen in the elongated receptacle of the recipient block, and obtaining a plurality of copies comprising sectioning the array transverse to the elongated donor specimen.
7. The method of claim 6, wherein the elongated donor specimen is placed in a receptacle having a cross-sectional size and shape complementary to a cross-sectional size and shape of the elongated donor specimen.
8. The method of claim 7, wherein forming the elongated receptacle comprises forming a cylindrical bore in the recipient block, and the donor specimen is obtained by boring a cylindrical tissue specimen from a donor block, wherein a diameter of the elongated receptacle is substantially the same as a diameter of the donor specimen.
9. The method of claim 1, further comprising associating a clinical or laboratory characteristic, or both, with each assigned location in the recipient array.
10. The method of claim 1 wherein performing the biological analyses comprises performing a different biological analysis on each copy.
11. The method of claim 10, wherein the different biological analyses are selected from the group consisting of at least an immunological analysis and a nucleic acid hybridization.

12. The method of claim 10, further comprising determining whether there are correlations between clinical or laboratory characteristics, associated with each assigned location, and the different biological analyses.

13. The method of claim 1, wherein the biological sample is a tissue specimen or cellular preparation.

14. The method of claim 12, wherein the clinical and laboratory characteristics are determined apart from performing the different biological analysis of each copy of the array; and the characteristics are one or more of patient age, tumor grade, tumor size, node status, and receptor status.

15. The method of claim 1, wherein placing the specimen in an assigned location in the array comprises placing a sample in a corresponding position of multiple copies of an array.

16. A method of parallel analysis of identical arrays of tissue specimens, comprising:  
forming a donor block comprising a biological specimen embedded in embedding medium;  
obtaining a plurality of elongated donor sample cores from the biological specimen;  
boring receptacle cores from a recipient embedding medium to form an array of elongated receptacles;  
placing the donor sample cores in the elongated receptacles at assigned locations in the array;  
sectioning the recipient embedding medium transverse to the elongated receptacles to obtain a cross-section of the donor sample cores in the array, while maintaining the assigned locations in the array in consecutive cross-sections;  
performing a different biological analysis of each cross-section; and  
comparing a result of each biological analysis in corresponding assigned locations of different sections to determine if there are correlations between the results of the different biological analyses at each assigned location.

17. The method of claim 16, further comprising comparing the results of the different biological analyses at each assigned location to clinical information about the biological specimen at the assigned location.

18. The method of claim 17, wherein the biological specimen is a tissue specimen from a tumor.

19. The method of claim 17, wherein the biological analyses are selected from the group consisting of a histologic analysis, an immunologic analysis, and a nucleic acid hybridization analysis.

20. The method of claim 17, wherein the results of the different biological analyses are compared to clinical information obtained about a subject from whom the biological specimen was obtained.

21. The method of claim 16, further comprising aligning a thin tissue section above the donor block to identify an area of interest from which the donor sample core is taken.
22. The method of claim 16, wherein the elongated donor sample core is a substantially cylindrical core that has a diameter that is less than about 1 mm.
23. A cross-section of the donor sample cores obtained by the method of claim 14.
24. The method of claim 1, further comprising using a nucleic acid microarray to identify a biomarker to be used in a biological analysis on the recipient array.
25. The method of claim 24, wherein the nucleic acid array is a cDNA or oligonucleotide microarray.
26. The method of claim 25, wherein the biomarker is selected by a high throughput immunological or genetic analysis.
27. The method of claim 24, wherein the biomarker comprises a marker for gene expression.
28. The method of claim 26, wherein the biomarker comprises a structural or numerical alteration of a chromosome, chromosomal region, gene, gene fragment or locus, or a gene function alteration.
29. The method of claim 1, wherein comparing the results comprises determining if there is an alteration of a gene by examining a marker for protein expression or other gene alteration.
30. The method of claim 29, wherein the alteration of protein expression is determined by an immunologic analysis.
31. The method of claim 29, wherein the alteration is an overexpression of vimentin in renal cell carcinoma, or an overexpression of IGFBP2 in human prostate cancer, or an overexpression of PDGFB in breast, lung, colon, testicular, endometrial or bladder cancer.
32. A method of analyzing genetic changes or gene expression in a tissue specimen, comprising:
  - screening multiple genes in a biological specimen, with a nucleic acid array that detects which genes are abnormally expressed in the biological specimen; and
  - screening multiple biological specimens in a biological specimen array, with a nucleic acid probe to detect which genes are abnormally expressed in the biological specimens;
  - wherein the result of screening multiple genes is used to select the nucleic acid probe to screen the multiple biological specimens, or wherein the result of screening multiple tissue specimens is used to select the array that detects which genes are abnormally expressed.
33. The method of claim 32, wherein screening multiple genes comprises performing a high throughput genomic technique.

34. The method of claim 32, wherein the high throughput genomic technique is selected from the group of cDNA or genomic DNA sequencing, protein sequencing, RDA, differential display, subtractive hybridization, SAGE, hybridization based sequencing, and cDNA and oligonucleotide arrays.

35. The method of claim 32, wherein screening multiple genes to determine which genes are abnormally expressed comprises searching databases and other biomedical sources of information.

36. The method of claim 32, wherein screening the multiple genes comprises using a cDNA array to determine which genes are abnormally expressed.

37. The method of claim 32, wherein screening the multiple genes comprises providing a DNA array which is assayed for a gene amplification, deletion, mutation, polymorphism, methylation change or other alteration of gene structure or function, or a genetic or molecular marker that reflects this change.

38. The method of claim 37, wherein the DNA array is a microarray that contains target loci that undergo differential expression in cancer.

39. The method of claim 32, wherein screening multiple genes obtained from a single biological specimen comprises hybridizing nucleic acid molecules associated with a cell with the DNA array that contains target loci that undergo differential expression, and determining which target loci indicate differential expression of a gene in the cell.

40. The method of claim 39, further comprising selecting a target locus that undergoes differential expression, providing a probe that includes or is complementary to at least a portion of the target locus, and using the probe to screen the multiple biological specimens.

41. The method of claim 32, wherein the biological specimen is a tissue specimen.

42. The method of claim 41, wherein the tissue specimen is a tumor specimen.

43. The method of claim 1, wherein the results of the different biological analyses are used to:

- a. evaluate a reagent for disease diagnosis or treatment;
- b. identify a prognostic marker for a disease;
- c. prioritize targets for drug development;
- d. assess or select therapy for a disease type; or
- e. find a biochemical target for medical therapy.

44. The method of claim 43, wherein evaluating a reagent for disease diagnosis or treatment comprises evaluating a reagent selected from the group of antibodies, genetic probes, and antisense molecules.



45. The method of claim 44, wherein evaluating a reagent for disease diagnosis or treatment comprises evaluating a reagent selected from the group of biological inhibitors, biological enhancers, or other biological modulators.

46. The method of claim 43, wherein identifying a prognostic marker for cancer comprises selecting a marker associated with a poor clinical outcome.

47. The method of claim 43, wherein selecting therapy for the subject comprises selecting an antineoplastic therapy that is associated with a particular biological analysis outcome.

48. The method of claim 47, wherein the particular biological analysis outcome is an oncogene amplification, deletion, translocation, mutation or other genetic rearrangement which is correlated with a clinical response to a particular therapy.

49. The method of claim 1, wherein the donor specimens are specimens from one or more tumors.

50. The method of claim 49, wherein the donor specimens are specimens from one or more tumors selected from the group of breast, prostate and bladder cancer.

51. The method of claim 49, wherein the donor specimens are specimens from a plurality of tumors all of the same organ or histologic type.

52. The method of claim 48, wherein the donor specimens are specimens from a plurality of tumors from different organs or tissue types.

53. A method of constructing a specimen array, comprising:  
providing cellular specimens in a matrix, with the specimens positioned at predetermined known positions, such that when multiple copies of the matrix are provided, a two dimensional array of specimens is presented on each copy, with each specimen at a predetermined position in the matrix, and wherein each matrix has a third dimension so that when sequential copies of the matrix are provided, the specimens maintain a predetermined relationship in the array; and

exposing sequential copies of the matrix to an agent which interacts with the specimens of the array, to identify those specimens which share a common biological property.

54. The method of claim 53, wherein the specimens are provided in an elongated form, and multiple copies of the matrix are made by cutting sections from a three dimensional array into predetermined sections, such that as sequential sections of the matrix are cut, the specimens maintain the predetermined relationship.

55. The method of claim 53, wherein the common biological property is a morphologic or molecular characteristic.

56. The method of claim 53, wherein the common biological property is a presence or absence, or altered level of expression, of a gene or protein, alteration of copy number, structure or function of a gene, genetic locus, chromosomal region or chromosome.

57. The method of claim 54, wherein the common biological property is a specific reaction with an antibody specific for a specimen of interest.

58. The method of claim 53, wherein the common biological property is correlated with an other characteristic of the specimens.

59. The method of claim 58, wherein the other characteristic of the specimens includes clinical information about a subject from whom each specimen was taken.

60. The method of claim 59, wherein the clinical information includes one or more of clinical course, treatment response, histological type or grade, tumor stage, age and sex of the subject from whom each specimen was taken.

61. The method of claim 53, wherein the cellular specimen is a tissue specimen.

62. The method of claim 53, wherein the cellular specimen is a cellular suspension.

63. The method of claim 62, wherein the specimen is a liquid cellular specimen that has been converted into a solid cellular specimen.

64. The array of claim 53.

65. The array of claim 54.

66. The method of claim 53, further comprising exposing a gene array to a candidate specimen, and selecting a candidate probe for the specimen array.

67. The method of claim 53, wherein the common biological property is her-2 status, and the method further comprises selecting a therapy based on her-2 status.

68. The method of claim 63, wherein the specimens comprise a tissue from a model or transgenic organism.

69. The method of claim 68, wherein the specimens comprise tissue from the model or transgenic organism at different stages of development.

70. The method of claim 53, wherein the specimens comprise animal, yeast or bacterial cells.

71. The method of claim 70, wherein the cells are in a liquid suspension which is applied to a surface of a support.

72. The method of claim 71, wherein the liquid suspension is from a body fluid.

73. The method of claim 72, wherein the body fluid is selected from the group of a needle aspiration, a cytology specimen, urine, and ascitic fluid.

74. The method of claim 70, wherein the cells comprise a sample of a liquid malignancy.

75. The method of claim 74, wherein the liquid malignancy comprises a hematological malignancy.

76. The method of claim 70, wherein the cells are from one or more cell lines.

77. The method of claim 53, wherein the specimens comprise specimens from one or more tumors at different stages of progression.

78. The method of claim 77, wherein the one or more tumors are prostate cancer tumors.

79. A method of screening for cancer in a specimen, comprising determining whether platelet derived growth factor beta (PDGFB), FGFR2, MYBL2, or IGFBP2 is expressed, overexpressed or amplified in the specimen.

80. A method of screening for cancer in a specimen, comprising determining:  
whether PDGFB is overexpressed or amplified in the specimen, wherein the cancer is selected from the group of lung, bladder and endometrial cancer;  
whether FGFR2 is amplified in the specimen, wherein the cancer is breast cancer;  
whether IGFBP2 is expressed in the specimen, wherein the cancer is hormone refractory prostate cancer;  
whether MYBL2 is amplified and expressed in breast cancer; and  
whether MYC, AR and cyclin-D1 are amplified in prostate cancer.

81. The method of claim 80, wherein the method comprises determining whether PDGFB is overexpressed or amplified in the specimen, wherein the cancer is selected from the group of lung, bladder and endometrial cancer.

82. The method of claim 80, wherein the method comprises determining whether FGFR2 is amplified in the specimen, wherein the cancer is breast cancer.

83. The method of claim 80, comprising determining whether IGFBP2 is expressed in the specimen, wherein the cancer is hormone refractory prostate cancer.

84. The method of claim 80, comprising determining whether MYBL2 is amplified and expressed in breast cancer.

85. The method of claim 80, comprising determining whether MYC, AR and cyclin-P1 are amplified in prostate cancer.